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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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October 14, 2005, 15:51:19; Search time 38.4375 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-10 29

1 TYAMH 5 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* A Geneseq 16Dec04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

uo	Anti-fact	Aspergill	Aspergill	Amino aci	HCV El an	HCV El an	Protein e	Pseudomon	Bacterial	Human OR-	Human olf	Human pro	A. oryzae	A. oryzae	Aspergill	Aspergill	Human imm	Peptide #	Peptide #	Human bon	Human bra	Human liv	٠.	Novel hum	Human DNA
Description	Aay79068	Aab14789	Aab14784	Aag65570	Abg76537	Abg76559	Abu24807	Abo77482	Adn27332	Aag72483	Aag71475	Adr10293	Aay50844	Aay50835	Aab14781	Aab14782	Aam82576	Abb40299	Aam33985	Aam73798	Aam61093	Abg55546	Abg43685	Aau18208	Abg92629
ΩI	AAY79068	AAB14789	AAB14784	AAG65570	ABG76537	ABG76559	ABU24807	AB077482	ADN27332	AAG72483	AAG71475	ADR10293	AAY50844	AAY50835	AAB14781	AAB14782	AAM82576	ABB40299	AAM33985	AAM73798	AAM61093	ABG55546	ABG43685	AAU18208	ABG92629
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ADC25346 ABG68752 ABG68752 ABG68718 ADE08218 ADE08219 ADA55412 ADA55412 ADA55412 ADA55412 ADA56014 ADA501014 AAG91014 AAG91014 AAG91014 AAG91014 ADF08003 ADF08003 ADF08003	ADE57186 ADE57190
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ALIGNMENTS

AAY79068 standard; peptide; 5 AA.

AAY79068;

(first entry) 12-JUN-2000 Anti-factor IX/IXa antibody H chain V domain CDR1 amino acid sequence.

Complementarity determining region 1, CDR1; antibody, Gla domain, factor IX/IXa, blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

09-MAR-2000

99WO-US019453. 26-AUG-1999; 98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC.

Kirchhofer D; Judice JK, Devaux B, Eaton DL, Hass PE, Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 1 (CDR1) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to two novel glutaminases (AAB14781, AAB14782) from Aspergillus oryae RRN616 and Aspergillus sojae BA-104 respectively which have molecular weights of approximately 73 kD (as determined by gel filtration). The enzymes have an optimum temperature of approximately 50 degrees Celsius, and an optimum pH of about 8.5. The glutaminases catalyee the conversion of L-glutamine to L-glutamic acid, and may be used in the production of fermented foodsruffs such as soy sauce and miso. Sequences AAB14787-B14789 represent fragments of Aspergillus oryzae KBN616 glutaminase which were used as the basis for the design of degenerate PCR primers AAA72205, AAA72207 and AAA72209. These primers were used in the isolation of genomic DNA encoding Aspergillus oryzae
cells and platelets. Compositions comprising the antibodies are used for the treatment or prophylaxis of thrombocit or cognilopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Glutaminase, Aspergillus oryzae KBN616; glutamic acid synthesis;
fermentation; foodstuff production; miso; soy sauce; peptide fragment;
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae KBN616 glutaminase peptide, SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 29; DB 3; Length 7; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                 Length 5;
                                                                                                                                                                                                          0; Indels
                                                                                                                                                                              100.0%; Score 29; DB 3; I
100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 25; 27pp; Japanese
                                                                                                                                                                                                                                                                                                                                    AAB14789 standard; peptide; 7 AA.
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                                                                                                                                                                 Query Match
Best Local Similarity 100.vv
Best Local Similarity 15.
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer design.
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                                                                                                                                                                                                                                     1 TYAMH 5
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                                                                                                                                                    Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determined for three V8 protease fragments (P1-P3) of Aspergillus oryzae KBN616 glutaminase in an exemplification of the invention
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                                                                                                                                                                                                                                                                                                         Aspergillus oryzae KBN616 glutaminase peptide fragment, SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                   Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis; fermentation; foodstuff production; miso; soy sauce; V8 protease digestion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new glutaminase and its preparation.
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                                                                                                                                                                 AAB14784 standard; peptide; 12 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus oryzae.
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les 5; Conserv
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                                  TYAMH
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1 TYAMH
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                                                                                                                                                                                                                AAB14784;
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virus

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Vaccine comprising a human monoclonal antibody against hepatitis C virus (HCV) El or E2 antigen, useful for treating or preventing HCV infection.
                                                                                                                                                                                                      1 TYAMH 5
                                                                                                                                              Sequence 121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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Best Local S
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                                                                                                                                                                                                                                           The invention relates to producing gene libraries, comprising immunoglobulin light and heavy variable region. The method involves selecting light chain that binds with the heavy chain product to produce a functional conformation, producing a gene library comprising a collection of these light chain variable genes, and combining with gene library of heavy chain variable genes. The method is used for production of gene and antibody libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, HCV, hepatitis C virus, El antigen, monoclonal antibody, vaccine,
hepatotropic, Fab, hypervariable region, E2 antigen, antibody.
                                                                                                                                                                         Producing gene libraries and antibody libraries, involves selecting a light chain that binds to a heavy chain product to produce a functional formation, and producing a gene library of the light chain variable
                                                                                                                 Shinohara M, Takahashi M;
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                                                                                                                                                                                                                                                                                                                                          100.0%; Score 29; DB 4; Length 120; 100.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCV El antigen monoclonal antibody #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG76537 standard; protein; 121 AA
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                                                                                                                                                                                                                          Examples; p 171; 181pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JAN-2001; 2001US-0260889P.
                                                                             22-FEB-2000; 2000JP-00050543.
                                                          22-FEB-2001; 2001WO-JP001298
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Best Local Si Conservative
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                                                                                                                Kurosawa Y, Akahori Y,
Okuno Y, Shiraki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-608502/65
                                                                                                                                              2001-565420/63
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TYAMH 35
                                                                                                                                                                                                                                                                                                                                                                                  1 TYAMH 5
                                                                                                                                                        N-PSDB; AAH47734
                                                                                                                                                                                                                                                                                                                        Sequence 120 AA;
                     WO200162907-A1
   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2002.
                                        30-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, HCV, hepatitis C virus, El antigen, monoclonal antibody, vaccine, hepatotropic, Fab, hypervariable region, E2 antigen, antibody.
                                                        The invention relates to a human monoclonal antibody or its antigen binding fragments, which exhibit immunological binding affinity for a hepatitis C virus (HCV) B1 antigen, comprising an amino acid sequence homologous to the binding portion of a human antibody Fab molecule from combinatorial antibody library. The vaccine composition comprising the antibodies or antigen binding fragments againet HCV B1 or R2 antigen or its hypervariable region is useful in treating or preventing HCV infection in a subject. Sequences ABG76513.ABG76568 represent human monoclonal antibodies against HCV B1 antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG76559 standard; protein; 128 AA.
Disclosure; Page 36; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KARO-) KAROLINSKA INNOVATIONS AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Persson MAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-608502/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 TYAMH 37
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                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                   Zyskind JW;
Xu HH;
         Gaps
         ö
                                                                                                                                                                                                                                                                                                   Ohlsen KL,
Forsyth RA,
         Indels
                                                                                                                                 Protein encoded by Prokaryotic essential gene #10334.
         ;
                                                                                                                                                                                                                                                                                                   Haselbeck R,
Yamamoto R,
77;
        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 52731; 1766pp; English.
Pred. No.
                                                                                ABU24807 standard; protein; 206 AA
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0
                                                                                                                                                                                                                                                                                                   Malone C,
Carr GJ,
                                                                                                                                                                                                                                         ; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
100.08;
                                                                                                                                                                                                                  21-MAR-2002; 2002WO-US009107,
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC.
         5; Conservative
                                                                                                                                                                  Clostridium botulinum
                                                                                                                                                                                                                                                                                                   Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                          WPI; 2003-029926/02
Similarity
                                        TYAMH 36
                        TYAMH 5
                                                                                                                                                                                                                                                                                                                                    N-PSDB; ACA28677
                                                                                                                                                                                 WO200277183-A2
                                                                                                                                                                                                                                         06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                   21-MAR-2001;
                                                                                                                                                                                                                                                                   06-MAR-2002;
                                                                                                                 19-JUN-2003
                                                                                                                                                                                                  03-OCT-2002
                                                                                                 ABU24807;
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                                         32
                                                                                                                                                                                                                                                                                                   Wang L,
Wall D,
Best Local
        Matches
                                                                 RESULT 7
                                                                          ABU24807
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The invention relates to an isolated mucietic actin comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid, conceding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation, or that this san activity against a biological pathway required for proliferation, or that inhibite scellular proliferation of an identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies to a agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene product is overszpressed or underexpressed; (12) determining the extent compound that inhibits proceduct for compound activity; (11) a culture comprising strains in which the gene compound acts; (9) manufacturing an antibiotic; (12) determining the extent compound that inhibits proceduct in overszpressed or underexpressed; (12) determining the extent compound activity is proceduct in a culture or collection of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational ö drug discovery programs, or for screening homologous nucleic acids invention relates to an isolated nucleic acid comprising any

Sequence 258 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-86884396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                  ö
                                                                                                                                                             Length 206;
                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                  ö
                                                                                                                                                               100.0%; Score 29; DB 6; I
100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 26228; 455pp; English.
                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rubenfield MJ, Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa polypeptide #9657.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                             ABO77482 standard; protein; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00252991.
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98US-0094190P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa.
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                                                                                                                                                                               Local Similarity
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TYAMH 34
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                                                                                                                               Sequence 206 AA;
                                                                                                                                                                                                                                      1 TYAMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                 ABO77482;
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                                                                                                                                                               Query Match
                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                              RESULT 8
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property comprises transformed plant, where the combinant DNA construct and growing the transformed plant with the percombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plants with construct and growing the transformed plant so increased resistance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of carbohydrate, nitrogen or homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                        Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; heat tolerance; plath disease resistance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
                                       Gaps
                                       ö
   Length 258;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goldman BS;
100.0%; Score 29; DB 7; L. 100.0%; Pred. No. 1.6e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 9985; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen X,
                                                                                                                                                                                                 ADN27332 standard; protein; 278 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                        Bacterial polypeptide #9985.
                                                                                                                                                                                                                                                                      (first entry)
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacterial polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-061375/06.
Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                        201 TYAMH 205
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                                                                        1 TYAMH
                                                                                                                                                                                                                                                                      02-DEC-2004
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                                                                                                                                                                                                                                     ADN27332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3acteria.
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(SLAT/)
(CHEN/)
(GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CAOY/)
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                                                                                                                                                              RESULT 9
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the present sequence is a polypeptide encoded by one of 344 newly mined human genes. It was used as a query sequence in a database search of charactory receptor (OR) like sequences. The invention relates to isolated polymucleotides encoding polypeptides involved in olfactory sensation.

The polymucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents primary scents. The methods also enable determination of secondary scents involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                                                                                                                                                 ö
production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html.
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
                                                                                                                                                                 ö
                                                                                                                             Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human OR-like polypeptide query sequence, SEQ ID NO: 2164.
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fuchs T,
                                                                                                                           100.0%; Score 29; DB 8; I 100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glusman G,
                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 1455-1456; 1857pp; English.
                                                                                                                                                                                                                                                                                                                                AAG72483 standard; protein; 307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lancet D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-OCT-2000; 2000WO-US027582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-1999; 99US-0158615P.
24-FEB-2000; 2000US-0184809P.
                                                                                                          Query Match
Best Local Similarity luv.
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-290713/30.
                                                                                                                                                                                                                                        220 TYAMH 224
                                                                                                                                                                                                      1 TYAMH 5
                                                                                           Sequence 278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200127158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bellenson J,
                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                    AAG72483;
                                                                                                                                                                                                                                                                                               RESULT 10
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DB 4; Length 307;

100.0%; Score 29;

Query Match

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New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                      human, oligo-capping method, diagnostic marker, gene therapy, osteoporosis, neurological disease, Alzheimer's disease; Parkinson's disease, dementia, short memory; cancer; sense or motor function; enocional reaction; fear response; panic; osteopathic, neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                              Human protein useful for treating neurological disease Seq 3799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 3799; 2686pp; English.
                                                                                                                                                                                                                                                                                                                                                             (REAS-) RES ASSOC BIOTECHNOLOGY,
                                                                                                                                                                                                                                                                                                                   14-FEB-2003; 2003JP-00102207.
09-MAY-2003; 2003JP-00131452.
                                                                                                                                                                                                                                                                                         12-FEB-2004; 2004EP-00003145.
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Isogai T, Yamamoto J,
Wakamatsu A, Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-583265/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADR08337
                                                                                                                                                                                                                                  EP1447413-A2.
                                                                                                                                                                             ranguiliser.
                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                               18-AUG-2004.
                                                    04-NOV-2004
                          ADR10293;
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              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antegonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                            Human, olfactory receptor, OR; primary scent determination, secondary scent determination; polypeptide library, odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yanai I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 29; DB 4; Length 321; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fuchs T,
                                                                                                                                                                                                                                  Human olfactory receptor polypeptide, SEQ ID NO: 1156.
           Pred. No. 1.9e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glusman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 674-675; 1857pp; English
                                                                                                                                                  AAG71475 standard; protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lancet D,
100.0%; Pre-
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(YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-2000; 2000WO-US027582.
                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0158615P
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                                                                                                                                                                                                        (first entry)
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           Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bellenson J, Smith D,
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Best Local Similarity
                                                                              154 TYAMH 158
                                                  1 TYAMH 5
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                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-1999;
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                                                                                                                                                                             AAG71475;
                                                                                                                      RESULT 11
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Otsuki T;

Nishikawa T, Isono Y, Sugiyama T, Nagai K, Irie R;

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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to constant obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antibodie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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AAY50844
ID AAY50
XX
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ADR10293 standard; protein; 531 AA.

RESULT 12

ADR10293 ü

169 TYAMH 173

g

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This invention describes a novel glutaminase enzyme isolated from Aspergillus oryzae which catalyses the decomposition of glutamine to glutamic acid and ammonia. The purified glutaminase and determined partial amino-acid sequence can be used for enhancing taste particularly in glutamic acid-converting food processing to give e.g. seasoning sauces and pastes as well as other seasoning materials. The gene thus obtained can be applied as probe for hybridization providing the gene-containing DNA fragments from genome and cDNA libraries of A. oryzae and A. nidulans, and subsequently modified glutaminase-producing breed. The novel strain of A. oryzae is a highly active because of its somatic secreting ability. This sequence represents the A. oryzae glutaminase enzyme described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus oryzae-originated glutaminase and partial amino-acid sequences for enhancing taste particularly in glutamic acid-converting food processing to make e.g. seasoning sauces and pastes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis; fermentation; foodstuff production; miso; soy sauce.
                Glutaminase, decomposition, glutamine, glutamic acid, ammonia; taste enhancer, seasoning, sauce, paste.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 29; DB 3; I 100.0%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                    1. .20
/label= signal_peptide
21. .690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus oryzae KBN616 glutaminase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim la; Page 41-44; 74pp; Japanese.
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB14781 standard; protein; 703 AA.
                                                                                                                                                                                                                                                                                                                                                                        98JP-00292443.
                                                                                                                                                                                                                                                                                              99WO-JP002455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-053292/04.
                                                                          Aspergillus oryzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 690 AA;
                                                                                                                                                                                                                 WO9960104-A1
                                                                                                                                                                                                                                                                                            12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koibuchi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2000
                                                                                                                                                                                                                                                                                                                                     15-MAY-1998;
11-SEP-1998;
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                                                                                                                                  Peptide
                                                                                                                                                                         Protein
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel glutaminase enzyme isolated from Aspergillus oryzae which catalyses the decomposition of glutamine to glutamine acid and ammonia. The purified glutaminase and determined partial amino-acid sequence can be used for enhancing taste particularly in glutamic acid-converting food processing to give e.g. seasoning sauces and pastes as well as other seasoning materials. The gene thus obtained can be applied as probe for hybridization providing the gene-containing DNA fragments from genome and CDNA libraries of A. oryzae and A. nidulans, and subsequently modified glutaminase-producing breed. The novel strain of A. oryzae is a highly active because of its somatic secreting ability. This sequence represents the A. oryzae glutaminase enzyme described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus oryzae-originated glutaminase and partial amino-acid sequences for enhancing taste particularly in glutamic acid-converting food processing to make e.g. seasoning sauces and pastes.
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                                                                                                               Glutaminase; decomposition; glutamine; glutamic acid; ammonia; taste enhancer; seasoning; sauce; paste.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kataoka J, Kitamoto K;
                                                                                                                                                                                                                                    1. .20
/label= signal_peptide
21. .690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 52-55; 74pp; Japanese.
                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagasaki H, Yuasa A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY50835 standard; protein; 690 AA
                                                                          A. oryzae glutaminase protein #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. oryzae glutaminase protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-00134080.
98JP-00258974.
98JP-00292443.
                                                                                                                                                                                                                                                                                                                                                                                               99WO-JP002455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-00089157
                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-053292/04.
                                                                                                                                                                         Aspergillus oryzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ43684
                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-1998;
11-SEP-1998;
14-OCT-1998;
                                   24-FEB-2000
                                                                                                                                                                                                                                                                                                                WO9960104-A1
                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koibuchi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-FEB-2000
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Gaps

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Matches

AAY5083

8X4X5X8

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Length 690;

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This sequence represents a novel glutaminase from Aspergillus oryzae KBN616. The invention relates to two novel glutaminases (AAB14781, AAB14782) from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which have molecular weights of approximately 73 kD (as determined by gel filtration). The enzymes have an optimum temperature of approximately 50 degrees Celsius, and an optimum BH of about 8.5. The glutaminases catalyse the conversion of L-glutamine to L-glutamic and an ye used in the production of fermented foodstuffs such as soy
               Location/Qualifiers
34. .703
/note= "Mature glutaminase; specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 29; DB 3; Length 703;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               A new glutaminase and its preparation.
                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 15-17; 27pp; Japanese.
                                                                                                                                              98JP-00347127.
                                                                                                                                                                                                           (AICH-) AICHI KEN PREFECTURE. (ICHI-) ICHIBIKI KK.
                                                                                                                                                                              98JP-00347127.
                                                                                                                                                                                                                                                            WPI; 2000-477931/42.
N-PSDB; AAA72204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 703 AA;
                                                                             JP2000166547-A.
                                                                                                                                              07-DEC-1998;
                                                                                                                                                                              07-DEC-1998;
                                                                                                              20-JUN-2000.
                Key
Protein
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Search completed: October 14, 2005, 16:12:37 Job time : 42.4375 secs

g ò

ö

0; Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein October 14, 2005, 16:02:59; Search time 6.95312 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-10 29 Title: Perfect score:

1 TYAMH 5 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Ig heavy chain V-I		adenylate kinase (conserved hypothet	hypothetical prote	tsh protein - Esch	hypothetical prote	끍	hypothetical prote	conserved hypothet	hypothetical prote	subtilis	8 YvpB	P450 3	P450	P450	cytochrome P450 3A	hypothetical prote		lysed fla			prot	fix23-3 protein -	probable helicase	hypothetical prote	integumentary muci	tha	Ig heavy chain V r
qi	M3HUGA	A35676	D71184	B83290	H71347	154632	T34500	150675	H86403	E90215	T22924	AD1165	AD1524	A29487	A34236	A34101	A25222	E82423	A84425	B64679	GNLJGA	GNLJGB	S29358	S18955	F84517	T21706	T30886	T30228	S26887
DB	ี่ ส	~	7	~	~	~	~	~	~	N	N	~	~	~	~	-	7	~	N	~	Н	Н	N	7	~	7	~	~	0
Length	122	138	196	249	1151	1377	95	196	213	222	228	242	242	501	501	502	504	609	723	801	852	852	852	996	1265	1385	1506	6260	35
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	86.2
Score	29	29	29	29	29	29	26	26	56	56	26	26	26	26	26	26	26	26	26	26	26	26	56	26	26	26	26	26	25
	-	7	e	4	Ŋ	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig heavy chain V r	leavy chain	neavy chain	neavy chain	leavy	eavy	neavy	able	leavy	neavy	Ig heavy chain V r	neavy chain	neavy chain	eavy	neavy chain	neavy chain
S46473	PL0120	S17609	S10385	S26885	526886	S29546	853076	PH1665	PH1653	PH1646	PH1644	PH1645	E33936	PH1667	846390
ın.	4	96	_	97 2				104 2						114 2	114 2
25 86.2	5 86.	Ŋ	5 86.	5 86.	5 86.2	5 86.2	5 86.2	5 86.2	5 86.2	5 86.2	5 86.2	5 86.2	5 86.2	5 86.2	5 86.2
30				34 2				38					43		

ALIGNMENTS

31 TYAMH 35 Ŋ 1 TYAMH

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RESULT 2
A35676
Ig heavy chain precursor V-D-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 23-Jul-1999
C;Accession: A35676
A;Accession: A35676; MUD:90287160; PMID:2113175
A;Accession: A35676
A;Accession: A35676
A;Residues: 1-138 *MHI>
A;Residues: 1-138 *MHI>
A;Residues: 1-138 *MHI>
A;Residues: 1-138 *MHI>
A;Coss-references: GB:M38066; NID:9185466; PIDN:AAA52974.1; PID:9553407
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <INM>

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hypothetical protein TP0245 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Species: 4-4-11-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: H71347
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDontey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: H71347
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1151 <COL>
A;Cross-references: UNIPROT:083273; GB:AE001206; GB:AE000520; NID:g3322514; PIDN:AAC6523<sup>3</sup>
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: 154632
R;Provence, D.L.; Curtiss, R.
A;Title: Immun. 62, 1369-1380, 1994
A;Title: Isolation and characterization of a gene involved in hemagglutination by an avi. A;Reference number: 154632; MUID:94178945; PMID:8132344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: pre: ininary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosidues: 1.137 cRES.
A;Kesidues: 1.137 cRES.
A;Cross-references: UNIRROT:047692; GB:L27423; NID:g469235; PIDN:AAA24698.1; PID:g469236.
C;Superfamily: IgA-specific metalloendopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross references: UNIPROT:023428; EMBL:U29244; PIDN:AAC71098.1; GSPDB:GN00020; CESP:ZK A;Experimental source: strain Bristol N2; clone ZK1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T3500
R;Latreille, P.
Submitted to the EMBL Data Library, June 1995
A;Reference number: 221534
A;Reference number: 221534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tsh protein - Bscherichia coli
C;Species: Bscherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Genetics:
A,Gene: TP0245
C,Superfamily: syphilis spirochete hypothetical protein TP0245
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A;Molecule type: DNA
A;Residues: 1-95 <LAT>
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Best Local Similarity 100.
Matches 5; Conservative
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T34500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ademylate kinase (EC 2.7.4.3) PH1753 [similarity] - Pyrococcus horikoshii
C; Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C; Accession: D71184
R; Kawarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir
M.; Ohfuku, Y; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. S, 55-76, 1998
A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A; Reference number: A71000; MUID:98344137; PMID:9679194
A; Reference number: A71000; MUID:98344137; PMID:9679194
A; Reterence number: A71000; MUID:98344137; PMID:9834314; PIDN:BAA30867.1; PID:9325
A; Resperimental source: strain O73
A; Note this accession replaces an interim accession for a sequence replaced by GenBank
C; Genetics:
A; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
B83290
conserved hypothetical protein PA2847 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: Ds. Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83290
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Loson, M.V.
Nature 406, 959-964, 200
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathcharter and the sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathcharter and the sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathchartus: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <STO>
A;Cross-references: UNIPROT: O9HZZ6; GB:AE004711; GB:AE004091; NID:g9948927; PIDN:AAG0623
A;Genetics:
A;Genetics:
A;Genetics:
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                                                      Length 138;
                                                                                                                                      0; Indels
                                                  Query Match 100.0%; Score 29; DB 2; Best Local Similarity 100.0%; Pred. No. 9; Matches 5; Conservative 0; Mismatches 0
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H71347
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Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative

||:|| TYSMH 16

1 TYAMH 5

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Conserved hypothetical protein [imported] - Sulfolobus solfataricus
Cispecies: Sulfolobus solfataricus
Cispecies: Sulfolobus solfataricus
Cipate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
Cidatession: E90215
Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-; Jong, II.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Appescription: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-222 «KUR»
A;Cross-references: UNIPROT:Q9UX67; GB:AE006641; NID:g13813846; PIDN:AAK40980.1; GSPDB:G
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A;Cross-references: UNIPROT:Q20984; EMBL:Z70754; PIDN:CAA94778.1; GSPDB:GN00023; CESP:F5*
A;Experimental source: clone F58E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1165
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22924
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A;Introns: 153/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Y75B12A.2
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80.0%; Pred. No. 78;
iive 1; Mismatches 0; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 2
Pred. No. 76;
1; Mismatches
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submitted to the EMBL Data Library, April 1996
A;Reference number: Z19638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Gene: SSO0678
C, Superfamily: hypothetical protein MJ0570
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Matches 4; Conservative
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202 TYALH 206
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AD1165
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86403
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Lin, X.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Titles: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; WUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNÅ
A;Residues: 1-196 <VIE>
A;Cross-references: UNIPROT:P41263; EMBL:X77960; NID:g457778; PIDN:CAA54922.1; PID:g4577
                                                                                                                                                                                                                                                                                                                                                                                                                retinol-binding protein precursor - chicken
Cippecies: Gallus gallus (Chicken)
Cippecies: Gallus gallus (Chicken)
Cippecies: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
CiDate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
CiDate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
CiDate: 13-Sep-1996 #sequence_revision 15-Sep-1996 #text_change 09-Jul-2004
Nyitle: Retinol in avian oogenesis: molecular properties of the carrier protein.
A;Reference number: 150675; MUID:95267350; PMID:7748490
A;Accession: 150675
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 73;
1; Mismatches 0; Indels
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80.0%; Pred. No. 67;
.ive 1; Mismatches 0; Indels
                                                                                           Score 26; DB 2; Length 95;
Pred. No. 32;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: lipocalin; lipocalin homology
F1-21/Domain: signal sequence #status predicted <SIG>
F36-195/Domain: lipocalin homology <LIP>
F36-191/91-195,141-150/Disulfide bonds: #status predicted
A;Map position: 2
C;Superfamily: Caenorhabditis elegans major sperm protein
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Best Local Similarity 80.0 Matches 4; Conservative

Query Match

C;Genetics:

|||:| 134 TYALH 138

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1 TYAMH 5

89.7%;

Query Match 89.7 Best Local Similarity 80.0 Matches 4; Conservative

1 TYAMH 5

A;Residues: 1-213 <STO>

A;Status: preliminary A;Molecule type: DNA

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396 TYALH 400
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AD1524
B. subtilis YupB protein homolog lin0732 [imported] - Listeria innocua (strain Clip11262 C; Species: Listeria innocua
C; Species: Listeria innocua
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C; Accession: AD1524
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Rccession: AD1524
A; Residues: Dreliminary
A; Molecule type: DNA
A; Residues: 1-242 < GGA>
A; Cross-references: UNIPROT:Q92DTO; GB:AL592022; PIDN:CAC95964.1; PID:g16413184; GSPDB:C
C; Genetics:
A; Genetics
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AZ9401. 1-3
Cytochrome P450 3A6 (version 1) - rabbit
Cytochrome P450 3A6 (version 1) - rabbit
NALternate names: cytochrome P450 3-3
N;Contains: oxidoreductase (EC 1.-...)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29487
R;Dalet, C.; Clair, P.; Daujat, M.; Fort, P.; Blanchard, J.M.; Maurel, P.
DNA 7, 39-46, 1988
A;Atcession: A29487
A;Title: Complete sequence of cytochrome P450 3c cDNA and presence of two mRNA species w
A;Reference number: A29487; MUID:88166352; PMID:3349903
A;Accession: A29487
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-501 cDAL>
A;Cross-references: UNIPROT:P11707; GB:M19139; NID:g165573; PIDN:AAA31430.1; PID:g165574
Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A,Title: Comparative genomics of Listeria species.
A,Reference number: AB1077; MUID:21537279; PMID:11679669
A,Accession: AD1165
A,Accession: AD1165
A,Status: preliminary
A,Molecule type: DNA
A,References: UNIPROT:Q87918; GB:NC_003210; PIDN:CAC98802.1; PID:g16410113; GSPDB:A;Cross-references: UNIPROT:G87918; GB:NC_003210; PIDN:CAC98802.1; PID:g16410113; GSPDB:G6netics:
A,Gene: Imo0724
C;Superfamily: Bacillus subtilis hypothetical protein yvpB
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Matches 4; Conservative
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191 TYSMH 195
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191 TYSMH 195
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A; Gene: CYP3A6
C; Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C; Superfamily: human cytochrom transfer; heme; iron; metalloprotein; monooxygenase;
F;301-462/Domain: cytochrome P450 homology <P45>
F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A34236
R;Potenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Griffin, K.J.; Schwab, G.E.; J. Biol. Chem. 264, 16222-16228, 1989
A;Title: Regulation of the rabbit cytochrome P-450 3c gene. Age-dependent expression and A;Reference number: A34236; MUID:89380226; PMID:2777787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-501 <POT>
A;Cross-references: UNIPROT:P11707; GB:J05034; NID:g164829; PIDN:AAA31178.1; PID:g164830
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N/Contains: oxidoreductase (BC 1.....)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CYP3A6
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein;
F;300-462/Domain: cytochrome P450 homology cP45>
F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted
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80.0%; Pred. No. 1.7e+02;
tive 1; Mismatches 0; Indels
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Pred. No. 1.7e+02;
1; Mismatches 0;
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80.0%;
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Best Local Similarity 80.0 Matches 4; Conservative
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Best Local Similarity 80.03
Matches 4; Conservative
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SEQUENCE
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                                                                                                                               October 14, 2005, 15:51:44 ; Search time 33.2812 Seconds (without alignments) 76.932 Million cell updates/sec
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096209
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q9HZZ6
Q9HZZ6
Q96ZC9
Q6N097
Q68CN4
Q68CN4
Q9HX9
Q9HX91
Q9HX31
Q9HX91
C9HX1
Q9HX91
Q9HX91
Q9HX91
Q9HX91
Q9HY92
Q9HY93
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Q86SK1
Q6LMV3
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Q9CKQ5
Q9CKQ5
Q9CG601
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Maximum Match 100%
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Q6XNP8
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                     020984
0887918
092dt0
0922t0
088723
08872
088572
07916
077916
065755
073181
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Nature 420:312-316(2002).
EMBL; AP003791; BAB90532.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                Q8Y918
Q92DT0
Q722H3
Q885K2
Q885K2
Q7Q8W1
Q7Q8W1
Q755K5
Q65K55
Q65K55
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01-JUN-2002 (TrEMBLrel. 21, Lis
01-OCT-2002 (TrEMBLrel. 22, Lis
B1065G12.14 protein.
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Gramene; Q8RZ81;
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KADA_PYRHO
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                                                                                              Query Match
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KADA PYRHO
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A SILVA A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Questive A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Questive A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Questive B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., Gamarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P., Caracili R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira R.C.C., Gruber A., Formighieri B.F., Franco M.C., Greggio C.C., Gruber A., Actsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Moreira L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D., Arindade dos Santos M., Truffi D., Tsai S.M., White F.F., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Romballia J.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D., Retubal J.C., Kitalima J.P.;

Romparison of the genomes of two Xanthomonas pathogens with differing RT host specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                ٠<u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                              MEDLINE=74175307; PubMed=4208843;
Florent G., Lehman D., Putnam F.W.;
"The switch point in mu heavy chains of human IgM immunoglobulins.";
Blochemietry 13:2482-2498(1974).
-!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 29; DB 1; Length 122; 100.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                              Ig-like.
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                 macroglobulin.
--- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A00502; MUGA.
PISP; PO1772; ZPB4.
GO; GO: 0005576; C: extracellular; NAS.
GO; GO: 0005872; P: entrigen binding; NAS.
GO; GO: 0005952; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                         122 122
122 AA; 13166 MW; 74E5B6959E84100A CRC64;
                                                                                                                                                                                                                                                                        PERM, PF00047; 19; 1.
SWART; SW00406; IGV; 1.
PROSITE; PS50815; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein XAC2050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=XAC2050;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
1es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Best Local S
Matches 5
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawarabayaai Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuqua H., Kikuchi H., Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 5:55-76(1998).
-1. CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
-1. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1. SIMILARITY: Belongs to the archaeal adenylate kinase family.
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                                                                                                                                                                                               100.0%; Score 29; DB 2; Length 158; 100.0%; Pred. No. 42; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
25-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)
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196 AA; 22413 MW; 26C834A1BE944D5F CRC64;
                                                                                                                                158 AA; 17289 MW; CIBIFB23AA6E930B CRC64;
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HSSP; P43410; IKI9.

HAMAP; MF 00234; -; 1.

ATP-binding; Complete proteome; Kinase; Transferase.

MP BIND 9 17 ATP (Potential).

SEQUENCE 196 AA; 22413 MW; 26C834A1BE944D5F CRC64
EMBL; AE011840; AAM36912.1; -.
InterPro; IPR001412; TRNA-synt I.
PR051TE; PS00178; AA_TRNA_LIGAŠE_I; UNKNOWN_1.
Complete protecome.
SEQUENCE 158 AA; 17289 MW; CIBIFB23AA6E930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=adkA; OrderedLocusNames=PH1753;
Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98344137; PubMed=9679194;
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Best Local Similarity 100...
Best Aca 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  132 TYAMH 136
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NCBI_TaxID=9606;
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MEDLINE-21349814; PubMed=11456446; DOI=10.1006/dbio.2001.0299;
WADIZENS, Spring J., Schmidli C., Schmid V.;
"Conservation of Hox/ParaHox-related genes in the early development of
                                                                                                                                        STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=2043737; Pubmed=10984043; DOI=10.1038/35023079;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino B., Weetbrook-Wadman S., Yuan Y., Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Patbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:00003700; F:transcription of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain_like.
InterPro; IPR000047; HTH_lambrepressr.
PF000046; Homeobox; 1.
                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription factor Cnox4-Pc.
Podocoryne carnea.
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
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                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 29; DB 2; Length 249; 100.0%; Pred. No. 67; O; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        Complete proteome; Hypothetical protein.
SEQUENCE 249 AA; 25989 MW; 8B24827650F64D6A CRC64;
                                   01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AA
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                         Created)
 PRT;
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PRINTS; PR00011; HTHREPRESSR.
SWART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
                                                                                                                                                                                                                                                                                           EMBL; AE004711; AAG06235.1; -.
                       (TrEMBLrel. 16,
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InterPro; IPR002781; DUF81.
Pfam; PF01925; DUF81; 1.
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NCBI_TaxID=6096;
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Best Local Similarity 10v...
Lag 5; Conservative
                                                                       OrderedLocusNames=PA2847;
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PRELIMINARY;
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                                                                                                                       NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a cnidarian.";
                       01-MAR-2001
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Q962C9
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Gaps
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686H20196.
Name-DKFZp686H20196;
Mame-DKFZp686H20196;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Human esophagus tumor;
The German Human cDNA Consortium;
Mambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                      100.0%; Score 29; DB 2; Length 356; 100.0%; Pred. No. 97;
                                                                                                                                                       0; Indels
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BAK40619; CAE45773.1; -.
HSSP; P01861; 1ADQ.
PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 356 AA; 41170 MW; EAF5E2308D76C6BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686E23209 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 29; DB 2; L
100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
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                                                                                                                                                          0; Mismatches
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INTERPRO; IPR003599; IG.
INTERPRO; IPR003109; IG_11ke.
INTERPRO; IPR003597; IG_21.
INTERPRO; IPR003596; IG_NC.
INTERPRO; IPR003596; IG_NC.
INTERPRO; IPR004596; IG_NC.
SWART; SW00409; IG_2.
SWART; SW00407; IGG1; 3.
SWART; SW00407; IGG1; 3.
FROSITE; PS002590; IG_LIKE; 4.
PROSITE; PS002590; IG_MHC; UNKNOWN_2.
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Matches 5; Conservative
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Galle R.F., Amanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Braton G.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., M. Brandon R.C., Rogers Y.H., Blazej R.G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Banos R.Y., Berman B.P., Baraktaroglu L., Beasley E.M., Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Autis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                              Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M., Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K., Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R., Klenk H.-P., "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
                  Probable acetyl-coenzyme A synthetase.
Name=acs; OrderedLocusNames=DP0825;
Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
                                                                                                                                                                                                                                                                                                                                                           from permanently cold Arctic sediments.";
Environ. Microbiol. 6:887-902(2004).
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-OCT-2004 (TrEMBLrel. 28, Last annotation update)
05-OCT-2004 (TREMBLrel. 28, Last annotation update)
03915-PB (GH270399)
Name=Drl-2; ORFNames=CG3915;
Name=brl-2; ORFNames=CG3915;
Bucaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 29; DB 2; Length 54 ilarity 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, CRS22870; CAG35554.1; -.
GO; GO:0003824; F:catalytic activity; IEA
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00154; AMPBINDING.
PROSITE; PS00455; AMP_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
                                                                                                                                                       [1] —
SEQUENCE FROM N.A.
STRAIN=LSv54 / DSM 12343;
PubMed=15305914;
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tes 5; Conserv
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           The German cDNA Consortium;

A losanger A., Fobo G., Han M., Wiemann S.;

Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,

Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,

L Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; CR749861; CAH18705.1; -.

R InterPro; IPR001599; Ig.

R InterPro; IPR001599; Ig.

R InterPro; IPR003997; Ig.-1.

R InterPro; IPR003997; Ig.-1.

R InterPro; IPR003996; Ig.-2.

R Pfam; PF00654; Cl-set; 3.

R Pfam; PF00671; ig. 4.

SMART; SM00407; IG; 2.

SMART; SM00406; IGV; 1.

R PROSITE; PS0835; IG LIKE; 4.

R PROSITE; PS0835; IG LIKE; 4.
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 493;
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STRAIN-APEC13;
Simose K.C., Delicato B.R., Gaziri L.C.J., Vidotto M.C.;
Submitted (ARE-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AV280856; AAP33781.1;
GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Peptidase S6.
InterPro; IPR009003; Peptidase S6.
Pfam; PP02395; IGAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 29; DB 2; Length 49.
100.0%; Pred. No. 1.4e+02;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 AA; 54117 MW; A1E4F5ED3FA8AB40 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tsh protein (Fragment).
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein
TISSUE=Rectum tumor;
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Q6AQ19;
25-OCT-2004 (
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Q83WR9

RESULT 9
10083MR9
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Best Loc Matches

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RESULT 10 Q6AQ19 ID Q6AQ19 AC Q6AQ19 DT 25-OC7

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Gaps

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Length 544;

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Hostin D., Houston K.A., Howland T.J., Meinandez J.K., Houston K.A., Howland T.J., Meinandez J.K., Houston K.A., Howland T.J., Wein M.H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lisako P., Lei Y., Lei Y., Lei Y., Lei Y., Lei Y., Liud D., Lia Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., M. McHarlana N.V., Mobarry C., Morris J., Moshrefi A., Monnt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Palazzolo M., Pitteman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M., Shue B.C., Spradling A.C., Stapleron M., Skupski M.P., Smith T., She B.C., Spradling A.C., Stapleron M., Skupski M.P., Smith T., Spradling A.C., Turner R., Venter B., Wang A.H., Wang X., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Weinstock G.M., Zhang G., Zaon Q.A., Yah R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhan G., Zhan G., Zhao Q., Zhao G., Weissenbach J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Kusso S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lewis S.E.; ^{\prime} "Annotation of the Drosophila melanogaster euchromatic genome: a
  Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Berkeley;
Stapleton M., Broketein P., Hong L., Agbayani A., Carlson J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2004)
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
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                                                      GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot_Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thammarongtham C., Turner G., Moir A.J., Tanticharoen M., Cheevadhanarak S.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                       ; Tyrosine-protein kinase.
71139 MW; 184FAA60CB84E457 CRC64;
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Last sequence update)
Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Glutaminase (EC 3.5.1.2).
                                                                                                                                                                                                                                                                                                                 100.0%; Score 29; DB 2; I 100.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                     Prodom; PD000001; Prot_Kinase; 1.
PROSITE; PS5011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN_1.
PROSITE; PS50814; WIF; 1.
Kinase; Transferae; Tyrosine-protein kinase.
SEQUENCE 648 AA; 71139 MW; 1B4FAARninearer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AY005477, AAG02575.1; -.
GO; GO:0004359; F:glutaminase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
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                                                                                                                                         InterPro; IPR001245; Tyr Dkinase.
InterPro; IPR008266; Tyr Dkinase AS.
InterPro; IPR003306; WIF.
EMBL; AE003820; AAF58429.3; -. EMBL; BT004493; AAO42657.1; -.
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Best Local Similarity 100.0%;
Matches 5; Conservative C
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                         HSSP; P08581; 1R1W.
FlyBase; FBgn0033791; Drl-2
                                                                                                                                                                                      Pfam; PF02019; WIF; 1.
PRINTS; PR00109; TYRKINASE.
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56 TYAMH 60
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Q9HGS1;
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                                                                                                                                               MEDLINE=22406523; PubMed=10952006;
Koibuchi K., Nagasaki H., Yuasa A., Kataoka J., Kitamoto K.;
"Molecular cloning and characterization of a gene encoding glutaminase
                                                                                                                                                                                                                                                                                                                                                                             Gaps
Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"The genome of fowlpox virus.";
"The Converse of 12000).
-i. SIMILARITY: Contains 14 ANK repeats.
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                                                                                                                                                                                                                                                                                                                                 Length 690;
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                                                                                                                                                                                                                      from Aspergillus óryzae.";
Appl. Microbiol. Biotechnol. 54:59-68(2000).
EMBL; AB029552; BAA86934.1; --
SEQUENCE 690 AA; 76164 MW; E3D0B17841EEA00D CRC64;
                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 29; DB 2; L.
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0;
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16-0CT-2001 (Rel. 40, Last sequence update)
05-JUU-2004 (Rel. 44, Last annotation update)
Putative ankyrin-repeat protein FPV222.
Name=FPV222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; Q60778; 10V3.

InterPro; IPR002110; ANK.

InterPro; IPR001810; P-box.

Pfam; PF000646; P-box; 1.

PRINTS; PR01415; ANK; 1S.

SMART; SM00248; ANK; 1S.

PROSITE; PS50297; ANK REP REGION; 1.

PROSITE; PS5098; ANK REP REGION; 1.

PROSITE; PS50088; ANK REP REGION; 1.
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NCBI_TaxID=10261;
                                                             NCBI_TaxID=5062;
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                                                                                                                                      STRAIN-RIB40;
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                                                                                                                                                                                                                                                    Gaps
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MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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                                                                                                                                                                                                   100.0%; Score 29; DB 1; Length 747; 100.0%; Pred. No. 2.1e+02;
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Complete protecome; Hypothetical protein.
SEQUENCE 1151 AA; 127556 MW; EDB635323CB4056 CRC64;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                               85303 MW; 55F90AF2855C3D28 CRC64;
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25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical protein TP0245.
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ANK 9.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
25-OCT-2004 (Rel. 45, Last ann
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Science 281:375-388(1998).
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nes 5; Conservative
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                                                                                                                                                    747 AA;
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TYAMH 5
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Sequence 45, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 18, Appl
Sequence 10284, A
Sequence 10284, A
Sequence 6294, Ap
Sequence 7091, Appl
Sequence 7091, Appl
Sequence 270, Appl
Sequence 21, Appl
Sequence 21, Appl
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                                                                                                                               October 14, 2005, 16:00:04; Search time 9.84375 Seconds (without alignments) 37.917 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-232-290-45

US-09-252-991A-26228

US-10-262-083-2

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US-09-270-767-35497

US-09-543-681A-8288

US-09-543-681A-8288

US-09-949-016-5992

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US-09-949-016-5992

US-09-919-038-10284

US-09-919-038-270

US-09-918-03148-26

US-09-138-091A-26

US-09-138-091A-26

US-09-138-091A-26

US-09-138-091A-26

US-09-424-840B-91

US-09-424-840B-91

US-09-270-7463-67

US-09-270-7465-8098-91

US-09-270-7465-91

US-09-270-7465-91

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US-09-271-202-118
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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US-09-23-290-45

Sequence 45, Application US/09232290A

Sequence 45, Application US/09232290A

Patent No. 6815540

GENERAL INFORMATION:

APPLICANT: NIEBA, LARS

APPLICANT: NIEBA, LARS

APPLICANT: NIEBA, LARS

APPLICANT: NIEBA, LARS

TITLE OF INVENTION: IMMONOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH

TITLE OF INVENTION: INCREASED SOLUBILITY

FILE REPRENCE: MORRHO/7

CURRENT APPLICATION NUMBER: US/09/232, 290A

CURRENT FILING DATE: 1999-01-15

SEARLIER APPLICATION NUMBER: PCT/EP96/02230
24, Appl
24, Appl
24, Appl
24, Appl
143, Appl
10, Appl
11, Appl
46, Appl
46, Appl
46, Appl
46, Appl
46, Appl
10, Appl
11, Appl
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APPLICANT: Bevaux, Brigitte
APPLICANT: Baton, Dan L.
APPLICANT: Hase, Philip E.
APPLICANT: Hase, Philip E.
APPLICANT: Suggett, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REPERENCE: Pi66IR2
CURRENT APPLICATION NUMBER: US/09/383,667
CURRENT FILING DATE: 1999-08-26
EARLIER PPLICATION NUMBER: US 60/098,233
EARLIER PILING DATE: 1999-08-28
EARLIER PLING DATE: 1999-03-03
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                                                                                                                                               US-08-545-809A-145
US-02-248-76A-14399
US-08-331-388A-46
US-08-561-521-12
US-08-561-521-13
US-08-551-521-13
US-08-331-397B-46
US-09-227-633-46
US-09-227-633-46
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100.0%; Pred. No. 4.1e+05;
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PCT-US95-01219-12
PCT-US95-01219-13
US-08-211-202-135
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Patent No. 6624295
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-383-667-10
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Best Local Similarity
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Sequence 18, Application US/10262083
Fatent No. 6830905
GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoko
APPLICANT: YUASA, Ari
APPLICANT: KATAOKA, Jiro
APPLICANT: KITAMOTO, Katsuhiko
TITLE OF INVENTION: A No. 6830905el Glutaminase, its Gene and a Method of Producing I
FILE REFERENCE: 199438US-8222-10-0-PCT
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
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                                                                                                                                                                                                    Length 690;
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100.0%; Pred. No. 1.1e+02;
ative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 690
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                                                                                                                                        , ORGANISM: Aspergillus oryzae
US-10-262-083-2
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                                                                                                                                                                                 Query Match
Best Local Similarity 100.
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Best Local Similarity
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                                                                                                                      TYPE: PRT
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Sequence 26228, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

PAPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 258
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Patent No. 6830905
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoko
APPLICANT: VUASA, Ari
APPLICANT: KATAOKA, Aisouhiko
APPLICANT: KATAOKA, Aisouhiko
TITLE OF INVENTION: A No. 6830905el Glutaminase, its Gene and a Method of Producing
FILE REFERENCE: 199438US-822-10-0-PCT
CURRENT APPLICATION NUMBER: US/10/262,083
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PRIOR APPLICATION NUMBER: US/09/674,507
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US/09/674,507
PRIOR PILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR PRIOR APPLICATION NUMBER: JP 11/89157
PRIOR FILING DATE: 1999-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT CORGANISM: Pseudomonas aeruginosa US-09-252-991A-26228
EARLIER FILING DATE: 1996-05-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45
LENGTH: 118
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Best Local Similarity luv..
Lac 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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201 TYAMH 205
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                                                                                              TYPE: PRT
; ORGANISM: Murine
US-09-232-290-45
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MS-09-543-681A-8288

Sequence 8288, Application US/09543681A

Sequence 8288, Application US/09543681A

Sequence 8288, Application US/09543681A

Sequence 8288, Application US/09543681A

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT PAPLICATION WUMBER: US/09/543,681A

CURRENT PILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR PILING DATE: 1999-04-09

NUMBER 0F SEQ ID NOS: 8344

SEQ ID NO 8288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26; DB 4; Length 455; Pred. No. 3.6e+02; 1; Mismatches 0; Indels
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Sequence 7091, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26; DB 4; Length 502
Pred. No. 3.9e+02;
1; Mismatches 0; Indels
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Best Local Similarity 80.0%;
Matches 4; Conservative
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; ORGANISM: Proteus mirabilis
US-09-543-681A-8288
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Best Local Similarity 80.0
Matches 4; Conservative
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398 TYALH 402
 152 TYALH 156
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US-09-949-016-5992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-949-016-5992
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Sequence 10284, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
APPLICANT: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 454
                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-270-767-50714

| Sequence 50714, Application US/09270767
| Sequence 50714, Application US/09270767
| Patent No. 6703491
| GENERAL INPORMATION:
| APPLICANT: Homburger et al.
| TITLE OF INVENTION: NACIEIC acids and proteins of Drosophila melanogaster:
| TITLE OF INVENTION: NACIEIC acids and proteins of Drosophila melanogaster:
| FILE REFERENCE: File Reference: 7326-094
| CURRENT FILING DATE: 1999-03-17
| NUMBER OF SEQ ID NOS: 62517
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 50714
| LENGTH: 108
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80.0%; Pred. No. 3.6e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                             Score 26; DB 4; Length 108;
Pred. No. 85;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.7%; Score 26; DB 4; Length 108; 80.0%; Pred. No. 85; 1.ve 1; Mismatches 0; Indels
                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-35497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa means any amino acid
                                                                       ORGANISM: Drosophila melanogaster FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Klebsiella pneumoniae
                                                                                                                                                               89.7%;
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35497
LENGTH: 108
                                                                                                                                              Query Match
Best Local Similarity 80.0.
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Best Local Similarity 80...
4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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TYALH 68
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US-09-489-039A-10284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATE: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.2%; Score 25; DB 1; Length 5; Best Local Similarity 80.0%; Pred. No. 4.1e+05; Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00
                                                                                                                                   ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 4113161CD1
US-09-919-039-270
                                                                                                                                                                                                                      89.7%; Score 26; DB 4; 1
80.0%; Pred. No. 4.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applic.
ATTORNEY/ACENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION:
                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
OPERATING SYSTEM: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Ce
STREET: 101 Richmond Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/08264093; Patent No. 5639863; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: not applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 868-1482
TELEPAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0-
        SOFTWARE: PERL Program
SEQ ID NO 270
LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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US-08-264-093-21
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ZIP: M5H 2J7
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US-08-918-148-26
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APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TILL OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT PILING DATE: 2000-10-12
PRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SEQ ID NO 699
LENGTH: 544
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR PLLING DATE: 2000-10-20
PRIOR PLLING DATE: 2000-10-03
PRIOR PLLING DATE: 2000-10-03
PRIOR PLLING DATE: 2000-10-03
PRIOR PLLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7091
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Beacht No. 6727066

GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REPERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401
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OTHER INFORMATION: Incyte ID No. 6673549 4113161CD1
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; Sequence 699, Application US/09976594
; Patent No. 6673549
                                                                                                                                                                                                                                                                                                                                                                                       89.7%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                US-09-949-016-7091
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; Sequence 26, Application US/08918148A
; Patent No. 634220
; GARREAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: Gurney, Augein L.
; APPLICANT: Gurney, Augein L.
; APPLICANT: Gurney, Augein L.
; APPLICANT: Pendly, Brian M.
; APPLICANT: Pendly, Brian M.
; APPLICANT: Gurney, Augein L.
; TITLE OF INVENTION: Agonist Antibodies
; TITLE OF INVENTION: Agonist Antibodies
; TITLE OF INVENTION: Agonist Antibodies
; TURERY FILING DATE: 1997-08-25
; VUMBER OF SEQ ID NOS: 79
; SEQ ID NO 26
; LENGTH: 5
; DRANISM: artificial
; PRATURE:
; NAME/KEY: 10D108CFv, 12B58CFv VH CDR1
; PRATURE:
; PRATURE:
; COTHER INFORMATION:
; COTHER INFORMATION:
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; ACCAITON: 1-5
; OTHER INFORMATION:
US-08-918-148-26

Query Match

Query Match

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps
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Search completed: October 14, 2005, 16:22:00 Job time : 10.8438 secs

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Sequence 64, Appl
Sequence 91, Appl
Sequence 25, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 31733,
Sequence 231272,
Sequence 231273,
Sequence 231273,
Sequence 231273,
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                                                                                                         October 14, 2005, 16:20:10; Search time 35:5469 Seconds (without alignments) 58.615 Million cell updates/sec
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1: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: \cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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6: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
7: \cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
8: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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22: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-11-0468-543-91
US-11-003-819-12
US-10-466-242-25
US-10-989-462-7
US-10-466-242-47
US-10-466-242-47
US-10-466-242-47
US-10-46-215-311733
US-10-282-122A-52731
US-10-282-122A-52731
US-10-989-462-34
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Maximum Match 100%
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Match Length
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Perfect score:
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Sequence 64, Application US/10889462

| Sequence 64, Application US/10889462
| Sequence 64, Application US/10889462
| Publication No. US20050220795A1
| GENERAL INFORMATION:
| APPLICANT: Wintrup, K. Dane
| APPLICANT: Yeung, Yik Andy
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: UNMBER: US 60/520,114
| PRIOR PPLICATION NUMBER: US 60/520,114
| PRIOR APPLICATION NUMBER: US 60/563,514
| PRIOR APPLICATION NUMBER: US
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sequence 25, Application US/10466242
Publication No. US20040208887A1
GENERAL INFORMATION:
APPLICANT: Drakenberg, Katarina
APPLICANT: Drakenberg, Katarina
TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
FILE REFERENCE: 0380-P032480500;
CURRENT APPLICATION NUMBER: US/10/466,242
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/SE02/00044
PRIOR PLING DATE: 2002-01-14
NUMBER OF SEQ ID NOS: 56
SSO ID NO 25
LENGTH: 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT WILTUP, K. Dane
APPLICANT WILTUP, K. Dane
TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01997-329001
CURRENT APPLICATION NUMBER: US/10/989,462
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/520,114
PRIOR PILING DATE: 2004-11-14
PRIOR PILING DATE: 2004-11-14
PRIOR PILING DATE: 2004-019
NUMBER OF SEQ ID NOS: 319
SOFTWARE: FASTEEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE
LOCATION: (1)..(121)
CTHER INFORMATION: Clone 2a:14 VH
US-10-466-242-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/10989462; Publication No. US20050220795A1; GENERAL INFORMATION:
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Best Local Similarity 100...
---- 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                  US-10-468-543-91

| Sequence 91, Application US/10468543 |
| Sequence 91, Application US/10468543 |
| Publication No. US20040091938A1 |
| GENERAL INFORMATION: |
| APPLICANT: Irimura, Tatsuro |
| APPLICANT: Mateumoto, Mariko |
| APPLICANT: Wim, Mijuug |
| APPLICANT: Wim, Mijuug |
| TILE OF INVENTION: Lectins for Analyzing Sugar Chains and Method of Using the Same |
| TILE NEFERRNCE: 03-786 |
| CURRENT APPLICATION NUMBER: US/10/468,543 |
| CURRENT FILING DATE: 2003-08-20 |
| PRIOR PLING DATE: 2001-02-20 |
| PRIOR FILING DATE: 2001-02-20 |
| SOFTWARE: PatentIn version 3.1 |
| LENGTH: 11 |
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| LENGTH: 11 |
| SEMICATION NO |
| SE
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| Bublication No. US2005015832A1
| GENERAL INFORMATION:
| APPLICANT: Evans, Elizabeth E. |
| APPLICANT: Sahasrabudhe, Deepak M. |
| FILE REFERENCE: 1843.019002
| CURRENT APPLICATION NUMBER: US/11/003,819 |
| CURRENT FILING DATE: 2003-12-04 |
| PRIOR APPLICATION NUMBER: US 60/256,572 |
| PRIOR APPLICATION NUMBER: US 60/256,572 |
| PRIOR APPLICATION NUMBER: US 60/531,688 |
| PRIOR FILING DATE: 2003-12-33 |
| NUMBER OF SEQ ID NOS: 61 |
| SEQ ID NO 12 |
| LENGTHE: PatentIn version 3.3 |
| LENGTHE: PatentIn version 3.4 |
| LENGTHE: PatentIn version
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US-10-468-543-91
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100.0%; Score 29; DB 20; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.1
Then 5; Conservative
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ORGANISM: Artificial
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US-10-466-242-25 RESULT 4

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**Sequence 211694, Application US/10425115

**Sequence 211694, Application US/10425115

**Publication No. US20040214272A1

**GENERAL INFORMATION:

**APPLICANT: La Rosa, Thomas J.

**APPLICANT: Cao, Yongwei

**TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

**TILLE OF INVENTION: Plants

**TILLE OF INVENTION: Plants

**TILLE OF INVENTION: Plants

**TILLE OF INVENTION: NUMBER: US/10/425,115

**CURRENT PILLING DATE: 2003-04-28

**NUMBER OF SEQ ID NOS: 369326

**SEQ ID NO 211694
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US-10-424-599-231272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: MRT4577_124664C.1.pep
US-10-425-115-211694
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NAME/KEY: unsure
LOCATION: (1)..(158)
OTHER INFORMATION: unsure at all Kaa locations
                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(151)
OTHER: INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
94;
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         CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 231272 LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Wall, Daniel
Trawick, John
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Best Local Similarity 100.
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Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
nes 5; Conservative
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ORGANISM: Zea mays
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APPLICANT:
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Matches
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Sequence 231272, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Carbu Yihua
APPLICANT: Cav Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
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APPLICANT: Persson, Mats
TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
TITLE REFERENCE: 0380-P03248US00
CURRENT APPLICATION NUMBER: US/10/466,242
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/SE02/00044
PRIOR FILING DATE: 2002-01-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Version 3.1
SEQ ID NOY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 29; DB 16; Length 128; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: MRT4577_47353C.1.pep
US-10-425-115-311733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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; OTHER INFORMATION: Clone 2b:5 VH
US-10-466-242-47
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100
5; Conservative
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
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Best Local S
Matches 5
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PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-03
PELLING DATE: 2001-03-09
PRIOR PELLING DATE: 2001-03-09
PRIOR PEL
                                 APPLICANT: Forsyth, R. APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER US/10/282,122A CURRENT FILLING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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FUDLication No. USZO050220795A1
GENERAL INFORMATION:
APPLICANT: Witterup, K. Dane
APPLICANT: Yeung, Yik Andy
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE REFERENCE: 01997-329001
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US/10/989,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 319
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 257
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Clostridium botulinum
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Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-989-462-34
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Sequence 9965, Application US/10369493
; Sequence 9965, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
    APPLICANT: Hinkle, Gregory J.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Willer Gregory J.
    APPLICANT: Goldman, Willer Gregory S.
    APPLICANT: Goldman, Willer Goldman, Barry S.
    APPLICANT: Goldman, Willer Goldman, Company Goldman, Barry S.
    APPLICANT: Goldman, Willer Goldman, Barry S.
    APPLICANT: Goldman, Willer Willer Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Willer Willer Willer Goldman, Barry S.
    FILE REFERENCE: 38-10(52052)B
    CURRENT FILING DATE: 2003-02-28
    PRIOR APPLICATION NUMBER: US 60/360,039
    PRIOR PRING DATE: 2002-02-21
    NUMBER OF SEQ ID NOS: 47374
    SEQ ID NO 9985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KOIBUCHI, Kyoko
APPLICANT: NAGASAKI, Hiroaki
APPLICANT: NAGASAKI, Hiroaki
APPLICANT: VARSA, AII
APPLICANT: KATAOKA, Jiro
APPLICANT: KATAOKA, Jiro
APPLICANT: KITAMOTO, Katsuhiko
TITILE OF INVENTION: A No. US230030170670Alel Glutaminase, its Gene and a Method of Prc
TITLE OF INVENTION: NUMBER: US/10/262,083
CURRENT APPLICATION NUMBER: US/10/262,083
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US-10-369-493-9985
  Mismatches
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PRIOR PELICATION NUMBER: US/09/674,507
PRIOR APPLICATION NUMBER: UP 10/134080
PRIOR PILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-09-11
PRIOR PELING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: UP 10/292443
PRIOR APPLICATION NUMBER: UP 11/89157
PRIOR APPLICATION NUMBER: UP 11/89157
PRIOR APPLICATION NUMBER: PCT/JP99/02455
PRIOR PILING DATE: 1999-03-30
PRIOR PILING DATE: 1999-05-12
PRIOR PLING DATE: 1999-05-12
PRIOR PLING DATE: 1999-05-12
PRIOR PLING DATE: 1999-05-12
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Publication No. US20030170670A1
GENERAL INFORMATION:
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; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-2
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Best Local Similarity 100.
  5; Conservative
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                                                                                                         31 TYAMH 35
                                                       1 TYAMH 5
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US-10-369-493-9985
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Gaps

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Query Match
100.0%; Score 29; DB 16; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels C
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: JP 10/258974
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1999-03-30
PRIOR PILING DATE: 1999-03-30
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-13
PRIOR PILING DATE: 1999-05-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-851-337-2
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US-10-262-083-18

US-10-262-083-18

Sequence 18, Application US/10262083

Publication No. US20030170670A1

GENERAL INFORMATION:

APPLICANT: NGASAKI, Hiroaki

APPLICANT: YUASA, Ari

APPLICANT: KATAOKA, Jiro

APPLICANT: APPL
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Sequence 2, Application US/10851337

Publication No. US2004022932A1

GENERAL INFORMATION:
APPLICANT: NOGENCH! Kyoko

APPLICANT: NAGASAKI, Hiroaki

APPLICANT: KATAOKA, Jiro

APPLICANT: KATAOKA, Jiro

APPLICANT: KATAOKA, Jiro

APPLICANT: KITAMOTO, Katsuhiko

TITLE OF INVENTION: Producing It

TITLE OF INVENTION: Producing It

CURRENT APPLICATION NUMBER: US/10/851,337

CURRENT APPLICATION NUMBER: US/10/262,083

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: US/10/674,507

PRIOR APPLICATION NUMBER: US/10/134080
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                                                                                    Length 690;
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                                                                       Query Match

100.0%; Score 29; DB 14;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 5; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US/09/674,507
PRIOR PILING DATE: 2000-11-15
PRIOR PILING DATE: 2000-11-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-11
PRIOR PILING DATE: 1998-05-11
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1998-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-13
PRIOR PILING DATE: 1999-03-13
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US-10-262-083-18
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Best Local Similarity 100.
Matches 5; Conservative
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- protein search, using sw model OM protein

Run on:

October 14, 2005, 15:51:19; Search time 130.688 Seconds (without alignments) 50.310 Million cell updates/sec

US-10-614-959-11 88 score:

1 IISYDGSKKYYADSVKG 17 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched: 2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp2000s:*geneseqp2001s:* geneseqp20048:* geneseqp1980s:* geneseqp1990s:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STEMMENTES

87	Match 100.0	Length	9 6	ID AAY79069	Description Aay79069 Anti-fact
	98.9	118	ß	ABB07230	Anti-1
87	98.9	248	Ŋ	ABP45312	Human
87	98.9	248	വ	ABP44905	Human
87	98.9	248	Ŋ	ABP44903	
87	98.9	248	7	ADG95730	
87	98.9	248	7	ADG95732	
87	98.9	248	7	ADG96139	
87	98.9	251	ß	ABP45103	
87	98.9	251	7	ADG95930	Adg95930 Single ch
98	7.76	135	7	ADD28319	Add28319 Human het
85	9.96	119	ហ	ABB07186	Abb07186 sHigM22 h
84	95.5	17	7	ABO33850	•
84	95.5	112	7	AB033836	
84	95.5	119	S	ABB07169	Abb07169 sHigM22 h
	95.5	119	œ	ADI26654	Adi26654 Human ant
83	94.3	17	٣	AAY79076	Aay79076 Anti-fact
83	94.3	123	æ	ADP22108	Adp22108 Human ant
83	94.3	125	7	ADE28443	Ade28443 Human ant
83	94.3	137	7	ADD28233	Add28233 Human het
83	94.3	137	7	ADD28321	Add28321 Human het
83	94.3	252	S	ABP45679	Abp45679 Human BLy
83	94.3	252	-	ADG96506	Adg96506 Single ch
83	94.3	470	7	ADE28467	_
83	94.3	614	ß	ABB06275	Abb06275 Plasmid R

	Abu56866 BONT/A Hc Aaw62799 Amino aci Aab40127 Anti-hIL1
2 AAW90298 3 AAX79074 3 AAX79078 5 AAX79078 7 ADJ32094 8 ADPH7199 8 ADSS255 8 ADSS2400 8 ADSS2400 8 ADSS2430 8 ADSS2430 8 ADSS2430 8 ADSS2430 8 ADSS2430 8 ADSS2430 6 ABSS62366 6 ABSS6237 6 AAX76976 6 ABUS68562 6 AAX76976 6 ABUS6837	6 ABU56866 2 AAW62799 3 AAB40127
7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	66 95 95
5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	82 93.2 82 93.2 82 93.2
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ALIGNMENTS

Complementarity determining region 2; CDR2; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA, inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence. AAY79069 standard; peptide; 17 AA (first entry) 12-JUN-2000 AAY79069;

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

99WO-US019453. 26-AUG-1999; 98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC.

Adams CW, Suggett S;

Kirchhofer D;

Judice JK,

Devaux B, Eaton DL, Hass PE,

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 2 (CDR2) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human antibody which binds human interleukin (IL)-4 receptor and is capable of inhibiting IL-4 induced biological activity, functions as IL-4 antagonist and is useful for treating septic arthritis, scleroderma.
the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angiopasery (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a human antibody (an interleukin (IL)-4 antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, antibody, interleukin, IL-4; antagonist, receptor, IL-4 receptor, antiarthritic, dermatological, antiulcer, antiinflammatory, cytostatic, antisickling, immunosuppressive, tuberculostatic, ophthalmological;
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Pred. No. 3.2e-07;
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15-FEB-2001; 2001US-00785934.
01-MAY-2001; 2001US-00847816.
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Matches 17; Conservative
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/note= "
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N-PSDB; ABA94330.
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inhibiting an IL-4-induced biological activity. (I) is also useful for inhibiting both IL-4-induced biological activity and IL-13-induced biological activity in a human, and for treating septic arthritis in a human afflicted with septic arthritis. (I) is also used for treating conditions such as septic/reactive arthritis, dermatitis herpetiformis, curicaria (especially formic idiopathic utricaria), ulcers, gastric inflammation, mucosal inflammation, ulcers, spatic, cinflammation, mucosal inflammation, ulcerstive colitis, Crohn's disease, inflammation, pays a role (e.g. IL-4-induced inflammation of part of the gastrointestinal tract), conditions in which IL-4-induced barrier colitis in which IL-4 plays a role (e.g. conditions characterized by decreased epithelial barrier function in the lung or gastrointestinal tract), scleroderma, hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to scleroderma, hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to medication, Kawasaki disease, sickle cell disease or crisis, Churg-Creationmune lymphoproliferative syndrome, autoimmune haemolytic anemia, strauss syndrome, drave's disease, pre-clampsia, Sjogran's syndrome, cutoimmune hymphoproliferative syndrome, autoimmune blastrosis, pemphigus vulgaris or bullous pemphigoid (autoimmune blastreing chaesase), and myasthenia gravis (an autoimmune muscular disease). IL-4 antagonists also find use as adjuvants to allery immunotherapy and as vacine adjuvants, especially when directing the immune response toward a THI response would be beneficial in treating or preventing the disease.
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2000US-0240816P.
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2001US-0277379P.
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Best Local Similarity 94.1
Matches 16; Conservative
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25-MAY-2001;
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ABP44903
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                                                                                                                                                   This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumphocyte Stimulator (BLyS) pupperides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and antibite each of a special proper immune, and autoimmune disorders and activity such as cancer, immune, rheumatorid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS). ABP41920-ABP47228 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                            Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                   Claim 1; Page 1981-1982; 3148pp; English
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17-OCT-2000; 2000US-0240BLGP.
16-MAR-2001; 2001US-027648P.
21-MAR-2001; 2001US-0277379P.
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25-MAY-2001; 2001US-0293499P.
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Matches 16; Conservative
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WPI; 2002-114799/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 248 AA;
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirhumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and soo may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be amountainstered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency and crammine (AIDS)). ABP43990-ABP4728 represent the antibodies and fragments of the antibodies described in the method of
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Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.9%; Score 87; DB 5; Length 248; 94.1%; Pred. No. 9.3e-06; ive 1; Mismatches 0; Indels
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                                                                                                                 Claim 1; Page 1495-1496; 3148pp; English.
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP44903 standard; protein; 248 AA.
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16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
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Best Local Similarity 94.1
Matches 16; Conservative
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1344 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single confain antibody molecules (screws) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The resemble invertion refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the abstrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This conjugation sequence date for this patent did not form part of invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format.

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                                                                                                                                                                                                                                                                               diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (cVID) and acquired immunodeficiency syndrome (AIDS)). ABP4399-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                 antibodies that immunospecifically bind to
                                                                                             B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in spiological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 87; DB 5; Length 248;
Pred. No. 9.3e-06;
1; Mismatches 0; Indels
                                                Claim 1; Page 1492-1493; 3148pp; English.
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                                                                                 This invention describes novel
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94.1%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 248 AA;
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                                                                                                                                                                                                                                                                                                                                                    the invention
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Gaps

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Length 248;

98.9%; Score 87; DB 7; Length 248 94.1%; Pred. No. 9.3e-06; ive 1; Mismatches 0; Indels

Conservative

Local Similarity les 16; Conserv

Query Match Matches

Sequence 248 AA;

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Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                             B cell proliferation; differentiation; scPv; myasthenia gravis; multiple sclerosis; aschma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritis; neuroprotective; antiinflammatory; antiaethmatic; antiallergic; cytostatic.
                                                                                                                                                                                    Single chain antibody that immunospecifically binds BLyS SeqID 916.
                                                                                                                                                                                                                 antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi GH, Vaughan TJ, Hilbert D;
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                                                                                                 ADG95732 standard; protein; 248
17
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19-DEC-2001; 2001US-0340817P.
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                  50 VISYDGSKKYYADSVKG
1 IISYDGSKKYYADSVKG
                                                                                                                                                          11-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM, Barash SC,
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                                                                                                                                                                                                                                                                                                       Unidentified
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Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 914; 394pp; English.

Vaughan TJ, Hilbert D;

Choi GH,

Ruben SM, Barash SC,

WPI; 2003-505530/47.

16-NOV-2001; 2001US-0331469P. 19-DEC-2001; 2001US-0340817P.

(HUMA-) HUMAN GENOME SCI INC.

14-NOV-2002; 2002WO-US036496,

10-JUL-2003.

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The Invention Fetaces to movel amiltonies that is a member of the tumour to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13d34 and encodes a protein that is a member of the tumour cerosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scrws) derived, preferably, from the variable chany can invention and differentiation. Specifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods contributed to the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders unclinding mysethenia gravis and multiple sclerosis, inflatmmatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and conjunction and proliferative disorders including leukaemia, carcinoma and conjunction and proliferative disorders including leukaemia, carcinoma and cartivities such as antirheumatic, antiathritis, infectious BLyS of the invention. NOTE: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format.

Change of the princed specification, but was obtained in electronic format.
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  invention relates to novel antibodies that immunospecifically bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.9%; Score 87; DB 7; Length 248; 94.1%; Pred. No. 9.3e-06; ive 1; Mismatches 0; Indels
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Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 248 AA;
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Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 1323; 394pp; English

Vaughan TJ, Hilbert D;

Choi GH,

Ruben SM, Barash SC, WPI; 2003-505530/47.

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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to CTromosome 1344 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scYes) derived, preferably, from the variable consistent thereof, of either human, murine, rat or monkey BLyS. The fragment thereof, of either human, murine, rat or monkey BLyS. The fragment thereof, of either human, murine, rat or monkey BLyS. The corresponding related to the aberrant expression or inappropriate function of BLyS or its receptor. As including mysathenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and laminama. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This antinflammatory, antiasthmatic, antiallergic and cytostatic. This invention. NOTE: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format cut be princed by the prince of the princed specification, but was obtained in electronic format.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.9%; Score 87; DB 7; I
94.1%; Pred. No. 9.3e-06;
iive 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human BLyS binding scFv SEQ ID 1114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP45103 standard; protein; 251 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 2000US-0240B16P.
; 2001US-027624BP.
; 2001US-0277379P.
; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0212210P.
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Best Local Similarity 94.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 248 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-2000; 2
17-OCT-2000; 2
16-MAR-2001; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001;
25-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CAMB-)
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chromosome 13934 and encodes a protein that is a member of the tumour chromosome 13934 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy (DTS region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammanory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as ALDS and proliferative disorders including leukaemia, carcinoma and cartivities such as antirheumatic, antiallergic and cytostatic. This printinflammatory, antiaethmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format che printed specification, but was obtained in electronic format chemets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human heterodimeric antibodies or their antibody fragments, useful as anti-toxins or anti-infectives with respect to infective agents, e.g. anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West Nile virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protective antigen, Bacillus anthracis, anthrax infection, cell receptedem factor; lethal factor; virucide; antibacterial; immunotherapy, anti-toxin, anti-infective; anthrax; botulinum; smallpox; verzuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human heterodimeric antibody heavy chain variable region SEQ ID NO:97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human heterodimeric antibody; human; antibody; binding affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 87; DB 7; I
Pred. No. 9.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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27-SEP-2002; 2002US-0414053P
25-NOV-2002; 2002US-0428807P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.9%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 VISYDGSKKYYADSVKG
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nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bowdish KS, Wild MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-722327/68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ното варіелв.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD28319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                HARAMA KARAKA KA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                            This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomdulatory, antirheumatic and antiAlDE activity of BLyS. The antibodies bind to Inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant ELyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatodia arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stimulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; B cell proliferation; atthmat; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritis; neuroprotective; antiinflammatory; antiarthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single chain antibody that immunospecifically binds BLyS SeqID 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.9%; Score 87; DB 5; Length 251 ilarity 94.1%; Pred. No. 9.4e-06; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hilbert D;
             diagnosis and treatment of cancers and immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaughan TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 1114; 394pp; English.
                                                                Claim 1; Page 1731-1732; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG95930 standard; protein; 251 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-0331469P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-505530/47.
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nes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 251 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Gaps

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Length 251; 0; Indels receptor;

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                                  The present invention describes a human heterodimeric antibody (I) fragment) having a binding affinity of at least 1x10-8 M to the protective antigen of Bacillus anthracis or a molecule involved in anthrax infection that blocks binding of the antigen or molecule to receptors, edema factor and lethal factor. (I) has virucide and antibacterial activities, and can be used in immunotherapy. The antibodies (I) are useful as anti-toxins or anti-infectives with respect to infective agents, such as anti-tax, botulinum, smallpox, Venezuelan equine encephalomyelltis virus (VEEV), or West Nile virus (WWV). The present sequence represents a human heterodimeric antibody heavy chain variable region amino acid sequence, which is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuromodulatory, central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.
                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                          Length 135;
                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                         97.7%; Score 86; DB 7; 94.1%; Pred. No. 6.8e-06;
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
            Claim 11; SEQ ID NO 97; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pease LR;
                                                                                                                                                                                                                                                                                                                                                                                          ABB07186 standard; protein; 119 AA
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                                                                                                                                                                                                                        Query Match
Best Local Similarity >---
Local 16; Conservative
                                                                                                                                                                                                                                                                                               1 IISYDGSKKYYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                        of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rodriguez M, Miller DJ,
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                                                                                                                                                                                                                 Sequence 135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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The invention provides a neuromodulatory agent (1) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS). (1) is capable of inducting remyelination, promoting cellular proliferation of gilal cells, and promoting Ca2+ signaling with oligodendrocytes. An humanised antibody to (1) can be selected from antibody sHIGM2 (LYM 22), ebvHigM MSI19D10, ebv HIGM CB2b68, AKJR4, CB2iEl2, CB2iE7 or MSI1955. (1) is useful for stimulating remyelination of CNS axons, stimulating proliferation of glial cells in

Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious

Claim 23; Fig 17; 219pp; English.

encephalomyelitis

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                                                                     TWEEV) Or for treating a human being having multiple sclerosis, or a human or domestic animal with a viral demyelinating disease, or a postneural disease of CNS. (T) is also useful for an in vitro method of stimulating the proliferation of glial cells from mixed cell culture. (I) is also useful for mixed cell culture. (I) is also useful for mixed cell culture. (I) stimulating the proliferation of glial cells from mixed cell culture. (I) stanso useful for stimulating remyelination of CNS axons. The antibodies are useful for preventing infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful for treating multiple sclerosis, Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating disease, CNS diseases, and other conditions in the CNS where nerves are chain variable region clone B amino acid sequence
CNS axons, or treating demyelinating disease of CNS in a mammal in need cf such therapy. (I) is aspable of binding to structures and cells within CNS. (I) is preferably useful for treating a demyelinating disease of CNS a mouse infected with Strain DA of Theller's murine encephalomyelities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an immunopolypeptide comprising a polypeptide that binds to human glucose-6-phosphate isomerase (GPI). The methods and compositions are used for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis. This is the amino acid sequence of human anti-GPI-antibody heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide; anti-GPI-antibody; GPI; glucose-6-phosphate isomerase; autoimmune disease; rheumatoid arthritis; heavy chain variable region; VH; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-GPI-antibody heavy chain complementarity determining region #10.
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                                                                                                                                                                                                                                                                                                                                                                                                                 96.6%; Score 85; DB 5; Length 119; 94.1%; Pred. No. 8.6e-06; 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-521517/49.
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BURTON D R.
SCHALLER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            Sequence 119 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB033850;
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Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious
                                                                   Neuromodulatory, central nervous system, CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIGM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.
                                              sHigM22 heavy chain variable region clone A sequence.
                                                                                                                                                                                                                                         (MAYO-) MAYO FOUND MEDICAL EDUCATION RES
                                                                                                                                                                                                                                                                Rodriguez M, Miller DJ, Pease LR;
                                                                                                                                                                                                                                                                                                                                                                                      Claim 23; Fig 17; 219pp; English.
                                                                                                                                                                                                                  10-MAY-2000; 2000US-00568351.
                                                                                                                                                                                           30-MAY-2000; 2000WO-US014902.
                       (first entry)
                                                                                                                                                                                                                                                                                       WPI; 2002-066596/09.
                                                                                                                                                                                                                                                                                                                                                               encephalomyelitis
                                                                                                                                                                                                                                                                                                    N-PSDB; ABA94216
                                                                                                                                            WO200185797-A1.
                                                                                                                      Homo sapiens
                       13-MAR-2002
                                                                                                                                                                    15-NOV-2001
 ABB07169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an immunopolypeptide comprising a polypeptide that binds to human glucose-6-phosphate isomerase (GPI). The methods and compositions are used for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis. This is the amino acid sequence of human anti-GPI-antibody heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunopolypeptide for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis, comprises a polypeptide that binds to human glucose-6-phosphate isomerase.
                                                                                                                                                                                                                                                                                       anti-GPI-antibody, GPI, glucose-6-phosphate isomerase, autoimmune disease, rheumatoid arthritis, heavy chain variable region,
                                                                                                                                                                                                                                                                           Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;
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                                                                       Gaps
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                                           Score 84; DB 7; Length 17;
Pred. No. 1.4e-06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                    Human anti-GPI-antibody heavy chain variable region #3.
                                                                     2; Mismatches
                                                                                                                                                                               ABO33836 standard; protein; 112 AA
complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schaller M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 3AH; 47pp; English.
                                                                                                           1 IISYDGSKKYYADSVKG 17
                                             95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2001; 2001US-00828708
                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2001; 2001US-00828708
                                                                                                                                                                                                                              (first entry)
                                                                      15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ditzel H, Burton DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-521517/49.
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                                             Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                               US2002146753-A1.
                       Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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Matches
                                                                       Matches
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The invention provides a neuromodulatory agent (I) capable of promoting central nervous system (CNS). (I) is capable of inducing remyelination, central nervous system (CNS). (I) is capable of inducing remyelination, promoting cellular proliferation of glial cells, and promoting Ca2+ signaling with oligodendrocytes. An humanised antibody to (I) can be selected from antibody sHIGMS2 (LVM 22), ebvHigh Mell9Dl0, ebv High CS2568, AKJR4, CB21E12, CB21E17 or MSI19E5. (I) is useful for stimulating remyelination of CNS axons, stimulating proliferation of glial cells in CNS axons, or treating demyelinating disease of CNS in a mammal in need of such therapy. (I) is capable of binding to structures and cells within CNS. (I) is preferably useful for treating a demyelinating disease of CNS. (CNS axons, or treating a human being having multiple sclerosis, or a post-onural disease of CNS. (I) is also useful for an in vitro method of chuman or domestic animal with a viral demyelinating disease, or a post-onural disease of CNS. (I) is also useful for stimulating remyelination of CNS axons. The antibodies are useful for stimulating remyelination of CNS axons. The antibodies continuating multiple sclerosis, Parkinson's disease, Alzheimer's condition or treating multiple sclerosis, Parkinson's disease, Alzheimer's disease, CNS diseases, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents the sHigM22 heavy condition variable region clone A amino acid sequence
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Pred. No. 1.3e-05;
2; Mismatches 0; Indels
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88.2%;
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ABB07169 standard; protein; 119 AA.

ABB07169 ID ABB0 XX

1 IISYDGSKKYYADSVKG 17

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
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OM protein - protein search, using sw model

Run on:

October 14, 2005, 16:02:59; Search time 23.6406 Seconds (without alignments) 69.190 Million cell updates/sec

US-10-614-959-11 88 Title: Perfect score:

1 IISYDGSKKYYADSVKG 17 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum

DB seq length: 0 DB seq length: 200000000 Maximum

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	heavy chain		chain	heavy	heavy chain	heavy	heavy	heavy	heavy	g heavy	g heavy	g heavy	heavy	g heavy	g heavy	g heavy	g heavy chain	g heavy	heavy	g heavy	g heavy	g heavy	heavy chain	g heavy	g heavy chain	heavy chain	g heavy	g heavy chain	Ig heavy chain -
SUMMARIES	ID	PL0120	844115	PL0116	S29546	PH1646	PH1644	PH1643	PH1645	S38490	S46390	S46392	836270	S31677	831116	F36005	831112	S19666	G36005	E36005	831119	S38493	PL0098	S31603	831679	S31674	831701	H16	46	н
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	% Query Match	93.2	e	93.2	3	3	3	3	3	m	m	3	3	3	m	n	m	r	m	m	m	m	m	ന	ന	m	~	n	S	85.2
	Score	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	77	75	75	75
	Result No.		7	e	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig heavy chain - h	heavy chain	chain	heavy chain	heavy chain											
831117	S48797	A49028	831510	S29543	836259	PH1662	M3HUAM	S31688	831598	S70442	A60943	S36284	PH1661	PH1660	831592
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122	128	133	133	96	117	118	122	134	135	140	151	115	121	118	92
85.2	85.2	85.2	85.2	84.1	84.1	84.1	84.1	84.1	84.1	84.1	83.0	81.8	81.8	80.7	78.4
		ñ	75	74	74	74	74	74	74	74	73	72	72	71	69
75	75	-													

ALIGNMENTS

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C;Accession: PL0120
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A;Reference number: PL0116; WUID:88286083; PMID:2840480
                                                                                       C;Species: Homo sapiens (man)
C;Date:`07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
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A;Accession: PL0120 A;Molecule type: mRNA A;Residues: 1-94 <BIR>

A;Cross-references: UNIPROT:QBWUK1; UNIPROT:Q9UL93
A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement f
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

Length 94; 93.2%; Score 82; DB 2; Length 94; ilarity 88.2%; Pred. No. 7.2e-06; Conservative 1; Mismatches 1; Indels Local Similarity les 15; Conserv Query Match

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Gaps

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19 heavy chain V region - human

19 heavy chain V region - human

19 c;Species: Homo sapiens (man)

2;Species: Homo sapiens (man)

2;Accession: S44115

3;Accession: S44115

3;Reference number: S44105

3;Reference number: S44105

3;Reference number: S44115

3;Residues: D17 *HAM>

3;Residues: L-97 *HAM>

3;Residues: L-97 *HAM>

3;Cross-references: EMBL: Z31384; NID: 9472969; PIDN: CAA83259.1; PID: 9940526

5;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Gaps ö Query Match
93.2%; Score 82; DB 2; Length 97;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels

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Ig heavy chain V region (clone 6H12) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PH1646
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hillson, J.L.; Karr, M.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1646
A;Molecule type: mRNA
A;Residues: 1-109 <HILL>
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R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1644
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R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Tille: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo A;Tele: The structural basis of permline-encoded NH3 immunoglobulin binding to staphylo A;Reference number: PH1642; MUID:93301610; PMID:8315388
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C,Species: Homo sapiens (man)
C,Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q8WUK1
C;Superfanily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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88.2%; Pred. No. 7.5e-06; ive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 82; DB 2; I
Pred. No. 8.4e-06;
1; Mismatches 1;
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93.2%; Score 82; DB 2; I
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1;
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88.2%;
                                                                                                                               50 VISYDGSNKYYADSVKG
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                                                                                         1 IISYDGSKKYYADSVKG
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Best Local Similarity 88.2.
Best Local Similarity 88.2.
                            15; Conservative
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A; Residues: 1-109 <HIL>
Best Local Similarity
                               Matches
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PLOLICE
PLOLICE
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens
CiAccession: PLO116; S26892
Ribitd, J.; Gallill, N.; Link, M.; Stites, D.; Sklar, J.
Skp. Med. 168; 229-245, 1388
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: PLO116; MUID:88286083; PMID:2840480
A;Reference number: PLO116; MUID:88286083; PMID:2840480
A;Residues: 1-98 AEIR>
A;Residues: 1-98 AEIRANDONIANIN V region; immunoglobulin homology
C;Reywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology
C;Reywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: domplementarity-determining 2
F;49-65/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    System of the property chain V region (COS-8 / DP-46) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: John-1994 # Hsequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29546; S2688B
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
A;Reference number: S29543
A;Reference number: S29543
A;Residues: 1-98 «TOM»
A;Residues: 1-98 «TOM»
A;Residues: BMBL:Z17394; NID:G32843; PIDN:CAA78997.1; PID:G32844
A;Residues: L-98 «TOM»
A;Residues: L-98 «TOM»
A;Residues: L-98 «TOM»
A;Residues: L-7776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V, A;Residues: S26885; MUID:93021117; PMID:1404388
A;Residues: Brellminary
A;Accession: S26888
A;Status: prellminary
A;Accession: S26888
A;Status: Prellminary
A;Residues: L-98 «TOD»
A;Cross-references: EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PID:G32913
A;Cross-references: EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PID:G32913
A;Cross-references: EMBL:Z12346; NID:G30911in homology
C;Keywords: heterotertamer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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Pred. No. 7.5e-06;
1; Mismatches 1; Indels
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Best Local Similarity 88.21
Matches 15; Conservative
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A; Molecule type: mRNA

1 IISYDGSKKYYADSVKG 17

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C,Accession: S36270
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, Emblers and J. S36256; MulD:93178448; PMID:7679990
A;Reference number: S36256; MulD:93178448; PMID:7679990
Ig heavy chain V region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: 846390
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A;Reference number: 846390, MUID:94254092; PMID:8196048
A;Accession: 846390
A;Accession: Stellminary
A;Accession: Speciminary
A;Greute: preliminary
A;Greute: Preli
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J. Mol. Biol. 239, 68-78, 1994
A.Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A; Reference number: $46392
A; Accession: $46392
A; Accession: preliminary
A; Status: preliminary
A; Residues: 1-114 <FIG>
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Homo sapiens (man)
C.Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C.Accession: S46392
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C'Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
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Pred. No. 8.8e-06,
1, Mismatches 1, Indels
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A;Residues: 1-117 <GRI>
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Pred. No. 8.8e-06;
1; Mismatches 1;
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50 VISYDGSNKYYADSVKG 66
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Local Similarity 88.2%;
nes 15; Conservative
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538490
Ig heavy chain - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: S38490
R; Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, R; Marks, J.D.; Ouwehand antibody fragments specific for human blood group antigens from a FA; Reference number: S38480
A; Reference number: S38480
A; Reference number: BABL Data Library, June 1993
A; Reference number: BABL Data Library, June 1993
A; Residues: BaBL: Z33030; NID: 3414027; FIDN: CAA80555.1; FID: 3414028
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; LS-98/Domain: immunoglobulin homology < NWM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PH1645

PH1645

PH1645

Grady chain V region (clone 6C8) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 24-Peb-1994 #sequence_revision 24-Peb-1994 #text_change 09-Jul-2004

C;Accession: PH1645

R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyld

A;Reference number: PH1642; MUID:93301610; PMID:8315388
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                                                        A;Residues: 1-111 <HIL>
A;Cross-references: UNIPROT:Q8WUK1
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:QBWUK1
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                               Length 111;
                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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1 IISYDGSKKYYADSVKG 17

A; Molecule type: mRNA A; Residues: 1-111 <HIL>

A;Accession: PH1645

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RESULT 10 S46390

Query Match Best Local Similarity 88.2° Matches 15; Conservative

Gaps

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Length 119; 1; Indels

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A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: P36005
                                                                                                                                                                                                                                                                   A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q22.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroteramer; immunoglobulin P:15-98/Domain: immunoglobulin homology <IMM>
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88.2%; Pred. No. 9.2e-06;
tive 1; Mismatches 1;
                                                                                                                                                                                      A;Cross-references: UNIPROT:Q8WUK1; GB:M34026
C;Genetics:
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Best Local Similarity 88.23
Matches 15; Conservative
                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
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S31116
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: 331116
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUDD:92111633; PMID:1730252
A;Accession: S31116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA
A;Residues: 1-118 - RRAA>
A;Cross-references: UNIPROT:Q8WUK1; EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                                     S31677

Ig heavy chain V region - human (fragment)

Ig heavy chain V region - human (fragment)

C; Species Homo sapiens (man)

C; Species Homo sapiens (man)

C; Accession: S31677

St. Ouishier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

St. Ouishinfer, A.M.; Gauthier, Library, June 1992

A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: S31585

A; Accession: S31677

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-118 < CUI>
A; Residues: 1-118 < CUI>
A; Cui>
A; Cui

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Superfamily: immunoglobulin

C; Keywords: heterotetramer; immunoglobulin
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              Score 82, DB 2; Length 117;
Pred. No. 9e-06;
1; Mismatches 1; Indels
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Pred. No. 9.1e-06;
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              Query Match
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25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Single-chain Fv (Fragment).
Name=scFv;
Name=scFv;
Buharyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Q652C9

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                                                    October 14, 2005, 15:51:44 ; Search time 113.156 Seconds (without alignments) 76.932 Million cell updates/sec
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Q8wuk1
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Q66093
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Q664Q7
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Q6mzu6
Q96bb9
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                         1612378 segs, 512079187 residues
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065ZC9
065ZC9
080UL1
090L90
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HV31 HUMAN
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HV05_CARAU
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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06in78
06mzq6
06gmx2
06gmx2
0920067
065z18
06997
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MEDINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MRD.X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                        OUTD3;
OHMY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AP035021; AAD56257.1; -.
PIR; PH1644; PH1644.
PIR; PL0120; PL0120.
HSSP; P01772; 2P84.
InterPro; IPR001110; Ig-like.
InterPro; IPR003110; Ig-v.
SWART; SM00406; IGv; 1.
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88.2%; Pred. No. 1e-05;
tive 1; Mismatches
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                                    HV3B HUMAN
Q920E7
Q65ZL8
Q6GPX4
Q9GJ71
Q9SU77
HV57 MOUSE
HV3C HUMAN
Q6N094
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ses 15; Conservative
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Length 613;

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PIR; PH1642; PH1642.

PIR; PH1643; PH1643.

PIR; PH1645; PH1646.

PIR; PH1646; PH1646.

PIR; PL0120; PL0120.

PIR; S1116; S31116.

PIR; S31119; S31119.

PIR; S31119.

PIR; S31119; S31119.

PIR; S31119.

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88.2%; Pred. No. 6.4e-05;
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MEDINE-2138257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2138257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2138257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MALSCHOLS R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haich F.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Haich F.,

A Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Marra M.A.,

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                 STRAIN=CIG/7;

MEDLINE=9736279; PubMed=9219263;

A Konternann R.E., Wing M.G., Winter G.;

Complement recruitment using bispecific diabodies.";

Nat. Biotechnol. 15:629-631(1997).

R BRBL; Y13056; CAA73499.1; -.

R InterPro; IPR001559; Ig.

R InterPro; IPR001596; Ig.

R Pfam; PF00047; ig; 2.

R SMART; SM00409; IG; 2.

R SMART; SM0406; IGv.

R PROSITE; PSS0835; IG_LIKE; 2.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020240; AH720240.1; -.
PIR; F36005; F36005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 240 25569 MW; FDCFD3645F64B373 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGHM protein.
Homo sapiens (Human)
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
       NCBI_TaxID=9606;
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBWUK1;
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Q8WUK1
       OX
RRY
RRY
RRY
RRY
DR RL
DR BDR
DR BDR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
WM X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 113;
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1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 113
113 AA; 12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
ERBL; AP035024; AAD56260.1; -.
PIR; S78486; S78486.
HSSP; POIT72; 2FB.4.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig-v.
START; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HV3G_HUMAN STANDARD; PRT; 122 AA P01768; 21-JUE-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update)
                                                                                                                                                                                                                             PRT;
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PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG MHC; UNKNOWN_2.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                         1 IISYDGSKKYYADSVKG 17
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22 VIAYDGSTQYYADSVRG 38
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                                                                                                                                                                                                                                                                        Local Similarity 70.6%;
les 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                        Query Match
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Matches
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(09Y509
TD (09Y5)
AC (09Y5)
DT (01-W
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                                                                                                                                                                                                                                                                                         MEDLINE-81013859; PubMed=6774332;
Lehman D.W., Putnam F.W.;
Lehman D.W., Putnam F.W.;
Location of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:2239-2243(1980).
-!- MISCELLANEOUS: This mu chain was isolated from the plasma of patient with macroglobulinemia.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02051; M3HUAM.
HSSP: P01772; 2FB4.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCDI_TaxID=9606;
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The German Human cDNA Consortium;
Mambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig-like.
Pyrrolidone carboxylic acid.
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Submitted (ANG-2003) to the BMBL/GenBank/DDBJ databases.
EMBL; BX640623; CAE45777.1; --
HSSP; P01061; 1ADQ.
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122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686104196 (Fragment)
Name-DKFZp686104196,
Hypothetical (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
05-JUL-2004 (Rel. 44, Last annotation update) Ig heavy chain V-III region CAM. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR005956; Ig-v.
Ffan; PF00047; ig: 1.
SMART; SM00406; IGv; 1.
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Interpro; IPR007110; Ig-11ke.
Interpro; IPR003597; Ig.C1.
Interpro; IPR003506; Ig.MC.
Interpro; IPR003596; Ig.WHC.
Interpro; IPR00554; C1-8et; 3.
SMART; SM00407; IGC1; 3.
SMART; SM00407; IGC1; 3.
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Best Local Similarity 70.0.
Best Local 2; Conservative
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NON_TER
SEQUENCE
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                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The German cDNA Consortium;

A Blocker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,

A Losanger A., PROD G., Han M., Wiemann S.;

Submitted (Add-2004) to the EMBL/GenBank/DDBJ databases.

R InterPro: IPRO03599; Ig. -

R InterPro: IPRO03599; Ig. -

R InterPro: IPRO03597; Ig.-1i.e.

R InterPro: IPRO03596; Ig.-V.

R InterPro: IPRO03506; Ig. WHC.

R InterPro: IPRO03506; Ig. V.

R Pfam, PPO0654; C1-set; 3.

R Pfam, PPO0644; Ig; 4.

SMART; SW00409; IG; 2.

R SMART; SW00409; IG; 2.

R PROSITE; PSS0835; IG_LIKE; 4.

R PROSITE; PSS0835; IG_LIKE; 4.

R PROSITE; PS080390; IG MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                    Length 417;
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                                    80.7%; Score 71; DB 2; Length 41.70.6%; Pred. No. 0.0029; Indels
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70.6%; Pred. No. 0.0052; Lindels
NON TER 1 1 SEQUENCE 417 AA, 46061 MW, C4518E844CFB883C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence upda
25-OCT-2004 (TrEMBLrel. 28, Last annotation up
25-OCT-2004 (TrEMBLrel. 28, Last annotation up
pyothetical protein DKFZp686EE33209 (Fragment)
Name=DKFZp686E23209;
                                                                                                                                                                                                                                                                                                                                                    493 AA.
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TISSUE-Mammary gland;
Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
HSSP; P01875; 10W0
                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934; DOI_10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 75.0%; Score 66; DB 2; Length 122; 1 Similarity 81.2%; Pred. No. 0.0053; 13; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWART; SM00406; IGV; 1.
PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 493 AA; 53224 MW; 12ECD7E094777101 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 AA; 13579 MW; 36054D41366545B8 CRC64;
                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.1%; Score 67; DB 2; 70.6%; Pred. No. 0.016; cive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035030; AAD56266.1; -.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGV; 1.
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                                                                                                                           Hypothetical protein FLJ90170.
Homo sapiens (Human).
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Interpro; IPR003597; Ig_cl.
Interpro; IPR003056; Ig_HHC.
Interpro; IPR003596; Ig_v.
Pfam; PF07654; Cl-set; Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Best Local Similarity
Matches 13; Conserv
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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ACCOCC OCT TO THE TRANSPORT OF THE TRANS
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DDT TO DD TO D
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                                                                                                                        Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
Lichtenstein A.K., Berenson J.R.;
"A CD10-positive subset of malignant cells is identified in multiple
myeloma using PCR with patient-specific immunoglobulin gene primers.";
Leukemia 9:1948-1953(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                      EMBL; S80860; AAD14339.1; -.
HSSP; PO1842; AAQ2
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
InterPro; PR0071316; Ig-like.
InterPro; IPR0071316; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Human rectum tumor; Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Bloecker H., Boecher M., Miemann S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BX538118; CAD98026.1; -. HSSP; P01857; 1HZH.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 67; DB 2; Length 482;
Pred. No. 0.016;
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SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8489FCAAA7BC925C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686N02209.
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PROSITE; PS00290; IG MHC; UNKNOWN_2.
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                                                                                            PubMed=7475288;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 AA; 15768 MW;
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50 LISYDGSTQYYAGSVKG 66
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70.6%;
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Best Local Similarity 76.5
Matches 13; Conservative
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Best Local Similarity
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                                                      SEQUENCE FROM N.A.
NCBI_TaxID=9606;
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SEQUENCE
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HV3H HVMAN STANDARD; PRT; 122 AA.
P0176;
P01776;
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V-III region GA.
IG heavy chain V-III region GA.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 12:7%; Score 64; DB 1; Length 122; Local Similarity 64.7%; Pred. No. 0.011; nes 11; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                       72.7%; Score 64; DB 2; Length 95; 75.0%; Pred. No. 0.0087; ive 1; Mismatches 3; Indels
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Pyrrolidone carboxylic acid.
PIR; S36280; S36280.
HSSP; P01820; 1G7J.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
NON_TER 1 1 1
NON_TER 95 95
SRQÜENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;
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122 AA; 13166 MW; 74E5B6959E84100A CRC64;
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-1-SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02052; MABUGA.
HSSP, P0172; ZRB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000855; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00710; Ig-like.
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SMART; SW00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
MEDLINE=74175307; PubMed=4208843;
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                                                                                                                                                                                                                                                                   Local Similarity 75.0
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SEQUENCE
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Обрла4;
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HV3H_HUMAN
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MEDLINE=79151016; PubMed=107164;
Putnam F.W., Liu Y.-S.V., Low T.L.K.;
Putnam F.W., Liu Y.-S.V., Low T.L.K.;
Putnam F.W., Liu Y.-S.V., Low T.L.K.;
Tigal protease, digestion, Fab and Fc fragments, and the complete amino acid sequence of the alpha 1 heavy chain.";
J. Biol. Chem. 254:2865-2874(1979)
J. Biol. Chem. 254:2865-2874(1979)
J. Biol. Chem. 254:2865-2874(1979)
R. A02056; AlHUBR.
RISSP, POIT72: PERP.
RO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
RO; GO:0005576; C:extracellular; NAS.
RO; GO:0000451; F:mmune response; NAS.
InterPro; IPR00110; Ig-like.
ROMANO, PERPO; IPR00110; Ig-like.
ROMANO, ROMANO, IG-LIKE.
ROMANO, ROMANO, IG-LIKE.
ROMANO, ROMANO, IG-LIKE.
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Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Imunoglobulin heavy chain (Fragment).
Enkaryota, Metazoa; (Dordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00406; ĬĠv; 1.
ROSSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Glycoprotein; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pyrrolidone carboxylic acid.
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB035268; BAA87067.1; -.
PIR; PH0872; PH08872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12981 MW; 12A709A75344D024 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-linked (GlcNAc. .).
                                                                                                                                                                                                                                       21-JJJ-1986 (Rel. 01, Created)
21-JJJ-1986 (Rel. 01, Last sequence update)
05-JJJ-2004 (Rel. 44, Last annotation update)
IIg heavy chain VIII region BUR.
Homo sapiens (Human).
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                             2 ISYDGSKKYYADSVKG 17
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nes 12; Conservative
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P01773;
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TISSUE-Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAGENER R.D., Felingold E.A., Grouse L.H., Derge J.G.,

MISCHILL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MALSCHOL S.F., Jeddan H., Moore T., Max S.I., Wang J., Haste F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Jodin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lux., Glibs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Maran A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Modriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Modriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Modriguez A.C., Marra M.A.;

Mara M.A., M.A., M.S., Marra M.A.;

Modriguez D.N., Marra M.A.;

Mandan J., Marra M.B.;

Mandan J., Marra M.B.;

Mandan
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                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO1847; AAH18747.1; -.
R HSSP; PO1864; 1ADO.
R InterPro; IPR007110; 1g-1ike.
R InterPro; IPR007110; 1g-1ike.
R InterPro; IPR007399; 1g-01.
R InterPro; IPR003906; 1g-MHC.
R InterPro; IPR003906; 1g-MHC.
R Pfam; PF07654; C1.set; 3.
SWART; SW00409; IG; 2.
SWART; SW00406; IGv; 1.
R PROSITE; PS50835; IG_LIKE; 4.
R PROSITE; PS50835; IG_LIKE; 4.
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SEQUENCE 470 AA; 51715 MW; 7B49556AllFD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches 12; Conservative
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                                                                                                                                                                                NCBI_TaxID=9606;
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Search completed: October 14, 2005, 16:19:51 Job time : 115.156 secs

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                                                                                                            October 14, 2005, 16:00:04; Search time 33.4688 Seconds (without alignments) 37.917 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-383-667-20

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Maximum Match 100%
Listing first 45 summaries
                                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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; Sequence 18, Application US/09383667
; Patent No. 6624295
; GENERAL INPORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Hass, Philip E.
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
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Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0;
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US-09-453-234-102
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US-09-453-234-110
US-08-862-124-17
US-08-862-124-14
US-09-560-198A-12
US-09-424-840B-113
US-09-560-198A-2
US-09-560-198A-2
US-09-560-198A-10
US-09-560-198A-10
US-09-560-198A-10
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US-08-899-575-81
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Patent No. 6624295
GENERAL INFORMATION:
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APPLICANT: Baton, Dan L.
APPLICANT: Baton, Dan L.
APPLICANT: Baton, Dan L.
APPLICANT: Baton, Dan L.
APPLICANT: Udisce, J. Kevin
APPLICANT: Suggett, Daniel
APPLICANT: Kirchhofer, Daniel
APPLICANT: Kirchhofer, Daniel
APPLICANT: Suggett, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                 Score 83; DB 4; Length 17;
Pred. No. 8.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.2%; Score 82; DB 4; Length 17; Best Local Similarity 88.2%; Pred. No. 1.2e-06; Matches 15; Conservative 1; Mismatches 1; Indels
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; Sequence 20, Application US/09383667
; Patent No. 6624298
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Baton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Hass, Philip E.
; APPLICANT: Xirchofer, Daniel
; APPLICANT: Suggett, Shelley
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                         0; Mismatches
           CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: P1661R2
CURRENT APPLICATION NUMBER: US/09/383,667
APPLICATION NUMBER: US/09/383,667
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Bercherdi, Peter
APPLICANT: Bercherdi, Peter
APPLICANT: Bercher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIB/IIIA RECOMBINANT ANTIBODIES
FILE REPERBNCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19620663.1
PRIOR APPLICATION NUMBER: DE 1975227.7
PRIOR PILING DATE: 1997-12-12
PRIOR PILING DATE: 1997-12-12
PRIOR PILING DATE: 1997-06-06
NUMBER: OF 128
SOFTWARE: PATENTING DATE: 1997-66-06
NUMBER: OF SEQ ID NOS: 128
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 36
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                     Query Match 93.2%; Score 82; DB 4; Length 17; Best Local Similarity 100.0%; Pred. No. 1.2e-06; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.2%; Score 82; DB 4; Length 17; Best Local Similarity 88.2%; Pred. No. 1.2e-06; Matches 15; Conservative 1; Mismatches 1; Indels
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APPLICANT: Berchtold, Peter
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: UB 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR PILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/038,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER APPLICATION NUMBER: US 60/122,767
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 36, Application US/09424840B; Patent No. 6790938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 95, Application US/09424840B Patent No. 6790938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VISYDGSNKYYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IISYDGSKKYYADSVK 16
                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-424-840B-36
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Sequence 118, Application US/08211202
Sequence 118, Application US/08211202
Patent No. 556332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: combinatorial approach
ITLE OF INVENTION: combinatorial approach
CORRESPONDENCES: 144
CORRESPONDENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Borun
STREET: 63100 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 1111nois
COUNTRY: USAA
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                                     Length 17;
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATE:
APPLICATION INMBER: US/08/211,202
FILING DATE: 23-SEE-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 82; DB 1; 1
Pred. No. 7.3e-06;
                                     Score 82; DB 4; 1
Pred. No. 1.2e-06;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATE: 25-SEP-1992
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: DAVIG W. CIOUGH
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
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36,107
..... 28111/31960
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INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                    1 IISYDGSKKYYADSVKG 17
                                                                                                                                          1 VISYDGSNKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.2%;
88.2%;
                                     Query Match 93.2%;
Best Local Similarity 88.2%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-211-202-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 60606-6402
  US-09-424-840B-108
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APPLICANT: BECHAIN, RODert F. A.
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT PILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 199663.1
PRIOR FILING DATE: 1998-05-08
PRIOR PELICATION NUMBER: DE 1975227.7
PRIOR PILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 1975227.7
PRIOR APPLICATION NUMBER: DE 1975227.7
PRIOR APPLICATION NUMBER: DE 1975227.7
PRIOR APPLICATION NUMBER: DE 197523904.8
PRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                    Query Match 93.2%; Score 82; DB 4; Length 17; Best Local Similarity 88.2%; Pred. No. 1.2e-06; Matches 15; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.2%; Score 82; DB 4; Length 17;
88.2%; Pred. No. 1.2e-06;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                        ; Sequence 97, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
                                                                                                                                                                                                                                          1 VISYDGSNKYYADSVKG 17
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
                                       ; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-424-840B-97
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Holliger, Kasper
APPLICANT: Holliger, Kasper
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Minter, Gregory
APPLICANT: Minter, Gregory
ITILE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 21389-001-28
FRICA APPLICATION NUMBER: US/09/726,219A
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT APPLICATION NUMBER: GB 9015188.6
FRICA APPLICATION NUMBER: GB 9012845.3
FRICA APPLICATION NUMBER: GB 9022845.3
FRICA APPLICATION NUMBER: GB 9024503.6
FRICA APPLICATION NUMBER: GB 910454.9
FRICA APPLICATION NUMBER: GB 910474.9
FRICA APPLICATION NUMBER: GB 910549.4
FRICA APPLICATION NUMBER: GB 910549.4
FRICA APPLICATION NUMBER: GB 910549.4
FRICA APPLICATION NUMBER: US 07/971,857
FRICA APPLICATION NUMBER: US 08/484,893
FRICA FILING DATE: 1993-01-08
FRICA APPLICATION NUMBER: US 08/484,893
FRICA FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SSOP ID NO 167
I-RNGTH: 115
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US-08-211-202-141
; Sequence 141, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
; APPLICANT: BAIER, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 82; DB 4; Length 115; 88.2%; Pred. No. 8.6e-06;
  1; Indels
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                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
1; Mismatches
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                                                                                                                                                                                                   Sequence 167, Application US/09726219A
Patent No. 6806079
                                                                                                                                                                                                                                                                                                                                                                               Johnson, Kevin
Hoogenboom, Hendricus
Griffiths, Andrew
                                                                    50 VISYDGSNKYYADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IISYDGSKKYYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Jackson, Ronald
  15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-167
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Matches 15; Conserv
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US-09-726-219A-167
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Matches
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APPLICANT: JISSERS, Laurent Stephane Anne Theree
HTHIE OF INVENTION: Production of chimeric antibodies - a
HTHE OF INVENTION: Combinatorial approach
NUMBERS OF SEQUENCES: 14
NUMBERS OF SEQUENCES: 15
NUMBERS OF SEQUENCES:
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93.2%; Score 82; DB 1; Length 119; 88.2%; Pred. No. 8.9e-06; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  i LOCATION: 1..119
GTHER INFORMATION: /note= "Human fetal immunoglobulin orther INFORMATION: 56P1'CL Variable Heavy chain (V-H)'US-08-331-398A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-0CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM
REGISTRATION NUMBER: 18,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 VISYDGSNKYYADSVKG 66
                                                                                                                                                                                                                                                                                   LENGTH: 119 amino acide
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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    FILING DATE: 30-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.2<sup>3</sup>
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
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APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David
APPLICANT: Fai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.2%; Score 82; DB 3; Length 117; 88.2%; Pred. No. 8.8e-06; ive 1; Mismatches 1; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/767,331
                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
OPERATING SYSTEM: Windows95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INPORMATION:
NAME: FREEMAN, ODEN W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46, Application US/08331398A Patent No. 5608039 GENERAL INFORMATION:
APPLICANT: Paten, Ira APPLICANT: Willingham, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELBEAX: 617-5-
TELEKX: 200154
; INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
"VPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.27
....hes 15; Conservative
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MOLECULE TYPE: protein
                                                                                       RY: US
02110-2804
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                                                                   STATE: M. COUNTRY:
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                                                              NAME/KEY: Protein

1.00ATION: 1.119

COTHER INFORMATION: /note= "Human fetal immunoglobulin OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ 1D NO: 46: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids TYPE: amino acid STRANDEDNESS: TOPOLOGY: linear NOLECULE TYPE: protein
                                                                                                                                      1 IISYDGSKKYYADSVKG 17
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US-08-759-804A-46
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TOPOLOGY: linear

MOLEGULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1.119

COTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"

OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"

OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"

OLIER INFORMATION: 56P1'CL VARIABLE (V-H)"

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1 IISYDGSKKYYADSVKG 17
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Sequence 262, App
Sequence 914, App
Sequence 1323, Ap
Sequence 914, App
Sequence 914, App
Sequence 1323, Ap
Sequence 1114, Ap
Sequence 1114, Ap
Sequence 1114, Ap
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                                                                                                                    October 14, 2005, 16:20:10; Search time 120.859 Seconds (without alignments) 58.615 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-880-748-914
US-09-880-748-914
US-09-880-748-914
US-10-291-418-914
US-10-293-418-1323
US-10-293-418-1323
US-10-293-418-1323
US-10-293-418-1114
US-10-989-462-276
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                                                                                                                                                                                                                                                                                                                                               1859788 segs, 416717961 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                            1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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US-10-989-462-300

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Sequence 916, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
-09-880-748-916
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| Publication No. US20030059937A1
| GENERAL INPORMATION:
| APPLICANT: Ruben et al.
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| FILE REFERENCE: PF23
| CURRENT FILING DATE: 2001-06-15
| PRIOR APPLICATION NUMBER: 60/212,210
| PRIOR APPLICATION NUMBER: 60/212,210
| PRIOR PILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-10-17
| PRIOR FILING DATE: 2000-10-17
| PRIOR FILING DATE: 2001-03-16
| PRIOR FILING DATE: 2001-03-16
| PRIOR FILING DATE: 2001-03-21
| PRIOR FILING DATE: 2001-03-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 121;
                                     Sequencial Application US/10989462
; Sequencian No. US20050220795A1
; GENERAL INFORMATION:
; APPLICANT: Wittrup, K. Dane
; APPLICANT: Wittrup, X. Dane
; APPLICANT: Wittrup, X. Dane
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 01997-329001
; CURRENT APPLICATION NUMBER: US/10/989,462
; CURRENT PILING DATE: 2004-11-15
; PRIOR PILICATION NUMBER: US 60/520,114
; PRIOR PPLICATION NUMBER: US 60/520,114
; PRIOR PPLICATION NUMBER: US 60/520,114
; PRIOR PLICATION NUMBER: US 60/53,514
; PRIOR PLICATION NUMBER: US 60/563,514
; RIOR PLICATION NUMBER: US 60/563,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.9%; Score 87; DB 18; Length 12
Best Local Similarity 94.1%; Pred. No. 1.2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IISYDGSKKYYADSVKG 17
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-914
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                                 -10-989-462-262
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Sequence 1323, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

ITILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 05/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PLING DATE: 2000-06-17

PRIOR PLING DATE: 2000-01-17

PRIOR PLING DATE: 2000-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PLING DATE: 2001-03-12

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239
GENERAL INVENTION:

GENERAL INVENTION: Antibodies that Immunospecifically Bind BLyS

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPRENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-61-15

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NOS: 329

SEQ ID NOS: 329

SEQ ID NOS: 329
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Pred. No. 2.5e-05;
1; Mismatches 0; Indels
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ilarity 94.1%; Pred. No. 2.5e-05;
Conservative 1; Mismatches 0;
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Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-916
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Best Local Similarity
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SEQ ID NO 1323
LENGTH: 248
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Gaps

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us-10-293-41b-1423

is Sequence 1323, Application US/10293418

publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-11-16

PRIOR PRILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-26

PRIOR FILING DATE: 2001-05-26

PRIOR FILING DATE: 2001-05-26

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-05-26

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2001-01-017

PRIOR FILING DATE: 2001-01-017

PRIOR FILING DATE: 2001-06-16

PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247
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publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PLLING DATE: 2000-6-15

PRIOR PLLING DATE: 2000-6-15

PRIOR PLLING DATE: 2000-6-15

PRIOR PLLING DATE: 2000-10-17

PRIOR PLLING DATE: 2000-10-17

PRIOR PLLING DATE: 2000-10-17

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PRIOR PLLING DATE: 2000-10-17
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                                                                       Score 87; DB 15; Length 248; Pred. No. 2.5e-05; 1; Mismatches 0; Indels
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Pred. No. 2.5e-05;
1; Mismatches 0; Indels
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FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
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                                                                             Query Match 98.9%;
Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 94.1%;
Matches 16; Conservative
; ORGANISM: Homo sapiens
US-10-293-418-916
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; ORGANISM: Homo sapiens
US-10-293-418-1323
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US-10-293-418-1323
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Sequence 916, Application US/10293418

Bublication No. US20030223996A1

GENERAL INFORMATION:

APPLICATY: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PFS23P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT PILING DATE: 2002-11-27

PRIOR PELING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-19

PRIOR FILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-05-25

PRIOR PELING DATE: 2001-05-25

PRIOR PELING DATE: 2001-05-25

PRIOR PELING DATE: 2001-05-25

PRIOR PELING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2000-10-17

PRIOR PELING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

LENGTH: 248

LENGTH: 248

LENGTH: 248
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GENERAL INFURNATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF223P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT PILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-02-19

PRIOR FILING DATE: 2001-02-15

PRIOR FILING DATE: 2001-02-15

PRIOR PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/210,616

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-010-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

LENGTH: 248

LENGTH: 248
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                                                                             ; Sequence 914, Application US/10293418; Publication No. US20030223996A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 16; Conserv
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US-10-364-743-97
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS23P2
CURRENT APPLICATION WHERE: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR PELING DATE: 2001-11-16
PRIOR PELING DATE: 2001-12-19
PRIOR PELING DATE: 2001-12-19
PRIOR PILING DATE: 2001-6-15
PRIOR PILING DATE: 2010-65-15
PRIOR PLING DATE: 2010-65-15
PRIOR PLING DATE: 2010-65-15
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2000-03-16
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Publication No. US20050220795A1
GENERAL INFORMATION.
APPLICANT: Wittrup, K. Dane
APPLICANT: Yeung, Yik Andy
TITLE OF INVENTION: ANTI-HYPROXYLASE ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01997-329001
CURRENT FILIAGE DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/520,114
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; Publication No. US20030223996A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1114
LENGTH: 251
                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-10-293-418-1114
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US-10-989-462-276
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APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
APPLICANT: Maruyama, Toshiaki
APPLICANT: Maruyama, Toshiaki
APPLICANT: Nolan, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 98 CTP (1087-73 CIP)
CURRENT APPLICATION NUMBER: US/10/452,593
CURRENT FILING DATE: 2003-06-02
PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/356,086
PRIOR FILING DATE: 2002-02-11
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APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Wild, Martha A.
APPLICANT: Wild, Martha A.
APPLICANT: Wo. US20040009178Alan, Mary Jean
TITLE OP INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)
CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR APPLICATION NUMBER: 125
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 97
LENGTH: 135
LENGTH: 135
                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-276
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US 60/563,514
PRIOR FILING DATE: 2004-04-19
NUMBER OF SEQ ID NOS: 319
SOFTWARE: RestSEQ for Windows Version 4.0
SEQ ID NO 276
LENGTH: 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97, Application US/10364743; Publication No. US20040009178A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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US-10-364-743-97
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| Sequence 24, Application No. US20550080239A1
| Sequence 24, Application No. US20550080239A1
| GENERAL INFORMATION:
| APPLICANT: Ditzel, H.
| APPLICANT: Button, D.
| APPLICANT: Button, M.
| TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil TITLE OF INVENTION: UNBER: US/10/630,009
| CURRENT FILING DATE: 2001-04-06
| NUMBER OF SEQ ID NOS: 123
| SOFTHARE: PASESEQ for Windows Version 4.0
| SEQ ID NO 24
| LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Button, D.
APPLICANT: Schaller, M.
APPLICANT: Schaller, M.
APPLICANT: Schaller, M.
APPLICANT: Schaller, M.
TITLE OF INVENTION: autoimmune disease
TITLE OF INVENTION: autoimmune disease
CURRENT APPLICATION NUMBER: 136.09/828,708
CURRENT APPLICATION NUMBER: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 17
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PRIOR APPLICATION NUMBER: US 60/376,408
PRIOR FILING DATE: 2002-04-29
PRIOR PILING DATE: 2002-04-29
PRIOR PILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIAN VEXBÍON 3.2
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/09828708
Patent No. US20020146753A1
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Matches 15, Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-630-009-24
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ORGANISM: human
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US-09-828-708-24
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US-10-630-009-24
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Query Match

Best Local Similarity 88.2%; Score 84; DB 17; Length 17;

Best Local Similarity 88.2%; Pred. No. 4.7e-06;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
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Search completed: October 14, 2005, 17:00:42 Job time : 121.859 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
          Copyright
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- protein search, using sw model protein ĕ

October 14, 2005, 15:51:19; Search time 84.5625 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-12 50

1 ASIAAARVLDY 11 score: Title: Perfect so Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 8 1 1 1 1 1 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:*geneseqp2000s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp1980s:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

	u	Anti-fact	Anti-fact	Oil-assoc	Human pol	Bacterial	Bacterial	Bacterial	Bacterial	Listeria	Zea mays	Zea mays	Amino aci	Bacterial	Arabidops	Arabidops	Sequence	Amino aci	Thermitas							
	Description	Aay79070	Aay79077	Adj48827	Aao13448	Ads26132	Ads25655	Ads25373	Ads22602	Abb48560	Aag18510	Aag18509	Aay37904	Ads28058	Aag20306	Aag51887	Aap80850	Aap80274	Aar54838	Aaw00768	Aaw00769	Aaw00774	Aaw00798	Aaw00770	Aaw00775	Aaw00780
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SUMMARIES	ID	AAY79070	AAY79077	ADJ48827	AA013448	ADS26132	ADS25655	ADS25373	ADS22602	ABB48560	AAG18510	AAG18509	AAY37904	ADS28058	AAG20306	AAG51887	AAP80850	AAP80274	AAR54838	AAW00768	AAW00769	AAW00774	AAW00798	AAW00770	AAW00775	AAW00780
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	f Query Match Length DB	11	11	408	28	652	652	655	959	708	157	159	180	231	237	237	278	279	279	279	279	279	279	279	279	279
d	Query Match	100.0	92.0	74.0	72.0	72.0	72.0	72.0	72.0	70.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0
	Score	50	46	37	36	36	36	36	36	35	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
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2 AAW00783 2 AAW00792 2 AAW00772 2 AAW00794 2 AAW00796 2 AAW00796 2 AAW00785 2 AAW00785 2 AAW00789	2 AAW00767 2 AAW00767 2 AAW00771 2 AAW00790 2 AAW00798 2 AAW00797
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2 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	8 0 0 1 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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Complementarity determining region 3; CDR3; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.
                                                             Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.
AAY79070 standard; peptide; 11 AA.
                                        (first entry)
                                        12-JUN-2000
                   AAY79070;
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Homo sapiens.

WO200012562-A1.

09-MAR-2000

99WO-US019453. 26-AUG-1999; 98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC.

Kirchhofer D; Judice JK, Devaux B, Eaton DL, Hass PE, Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 3 (CDR3) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, atterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PYCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity determining region 3; CDR3; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastesis; percutaneous transluminal coronary angioplasty; PTCA; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kirchhofer D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.
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0
                                                                                                                                                                                                                                           Length 11;
                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                           Score 50; DB 3;
Pred. No. 0.003;
Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY79077 standard; peptide; 11
                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US019453
                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                 ASIAAARVLDY 11
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                                                                                                                                                                                                                                                                                                                1 ASIAAARVLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-256595/22.
                                                                                                                                                                                                          Sequence 11 AA;
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03-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY79077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams CW,
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant DNA construct comprising a promoter functional in
plants operably linked to an oil-associated gene for producing transgenic
indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Length 408;
                                                                                                                                                      Length 11;
                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ledeaux JR,
                                                                                                                                                    Score 46; DB 3;
Pred. No. 0.019;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
62;
                                                                                                                                                                                                                                                                                                                                                                                                        Oil-associated gene related protein #327.
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score Pred. 1
                                                                                                                                                                                                                                                                                                                  ADJ48827 standard; protein; 408 AA.
                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2002; 2002US-0365301P.
26-JUN-2002; 2002US-0391786P.
26-JUN-2002; 2002US-0392018P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.0%;
80.0%;
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                                                                                                                                                      92.0%;
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ravanello M,
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                               1 ASIAAARVLDY 11
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                                                                                                                                                                                                                                          1 ASIAAGRVLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAURIE C C.
RAVANELLO M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEDEAUX J R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-142683/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROGERS J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAVAGE T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 408 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2004025202-A1.
                                                                                                                          Sequence 11 AA;
                                                                                                                                                      Query Match
Best Local Simil
Matches 10; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant seed
                                                                                                                                                                                                                                                                                                                                                ADJ48827;
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(LEDE/)
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                         Recombinant DNA construct, transformed plant; improved plant property; cold tolerance; heat tolerance; heat tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                 Bacterial polypeptide #15165.
                                                                                                                                                                                                                                                                                   20-FEB-2003; 2003US-00369493.
                                                                                                                                                                                                                                                                                                              21-FEB-2002; 2002US-0360039P.
                                       02-DEC-2004 (first entry)
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                                                                                                                                                                                                                               US2003233675-A1.
                                                                                                                                                                                                                                                          18-DEC-2003
                                                                                                                                                                                                     Bacteria.
              ADS26132
                                                                                                                                                                                                                                                                                                                                         (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                              (GOLD/)
                                                                                                                                                                                                                                                                                                                                                                   (SLAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                         Cao Y,
                                                                                                                                                                                                                                                                                                                                                       (HINK/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, c.g. stem cell growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 27340; 1399pp + Sequence Listing; English.
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Pred. No. 12;
2; Mismatches 1; Indels
 Indels
 1;
Mismatches
                                                                                                                    AA013448 standard; protein; 58 AA.
                                                                                                                                                                                                    Human polypeptide SEQ ID NO 27340.
 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fang YT, Liu C, Drmanac RT
                                                                                                                                                                          (first entry)
8; Conservative
                                          ||:|||| ||
275 ASLAAARALD 284
                          10
                          1 ASIAAARVLD
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N-PSDB; AAI93379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                              WO200164835-A2
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001.
                                                                                                                                                AA013448;
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 Matches
                                                                                                         RESULT
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Goldman BS;

Chen X,

Slater SC,

Hinkle GJ,

CAO Y. HINKLE G J. SLATER S C.

GOLDMAN B S

CHEN X.

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant cauch as maize or soybean. The method of producing a transformed plant cannot be an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the collyncheotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmotic conditions or properties.

The recombination of plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, introgen or providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the scome of the printed specification but was obtained in electronic forms. From the print of the printed specification the printed spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  format from USPTO at segdata.uspto.gov/sequence.html
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Pred. No. 1.6e+02;
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Claim 1; SEQ ID NO 15165; 122pp; English.
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Best Local Similarity 63...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 652 AA;
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1 ASIAAARVLDY 11

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ADS26132 standard; protein; 652 AA.

RESULT 5 ADS26132

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Gaps

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Best Local Similarity 70.(Matches 7; Conservative

2 SIAAARVLDY 11

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21

|:| |||||| SVAQARVLEY

12

Sequence 652 AA;

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The invention is relates to a recommendate the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for improved plant properties. Colerance to herbicides, extreme osmocit conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth requiators, increased rate of content, improved yield by modification of carbohydrate, introgen or phosphorus use and/or uptake, by modification of carbohydrate, introgen or providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan completion production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic correction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                     Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a recombinant DNA construct comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goldman BS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 14688; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen X,
                                                                                                             ADS25655 standard; protein; 652 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                               Bacterial polypeptide #14688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2002; 2002US-0360039P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                 (first entry)
255 AATAAARAIDY 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAO Y.
HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-061375/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOLDMAN B S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHEN
                                                                                                                                                                                                 02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2003.
                                                                                                                                                       ADS25655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GOLD/)
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                                                                                        ADS25655
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant cauch as maize or soybean. The method of producing a plant with the carecombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with construct is useful for improved plant properties. The recombinant DNA construct is useful for improved plant properties. Conteased cold, heat or drought tolerance, colerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth rate by modification of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant DNA construct comprising a promoter positioned to provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                     cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct; transformed plant; improved plant property;
                                                        Gaps
                                                        ö
                  Length 652;
              Score 36; DB 8; Length 652
Pred. No. 1.6e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 14406; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen X,
                                                                                                                                                                                                                                ADS25373 standard; protein; 655 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Slater SC,
                                                                                                                                                                                                                                                                                                                                                Bacterial polypeptide #14406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2002; 2002US-0360039P
                  72.0%;
63.6%;
                                                                                                                                                                                                                                                                                                        02-DEC-2004 (first entry)
                                                          Conservative
                                                                                                                  |: |||| :||
255 AATAAARAIDY 265
                                                                                            1 ASIAAARVLDY 11
Query Match
Best Local Similarity
7; Conserv?
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SLATER S C.
CHEN X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003233675-A1.
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                                                                                                                                                                                                                                                                      ADS25373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HINK/)
                                                                                                                                                                                          RESULT 7
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providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
   888888888
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Sequence 655 AA;

Gaps ; 0 72.0%; Score 36; DB 8; Length 655; 63.6%; Pred. No. 1.6e+02; ive 2; Mismatches 2; Indels 63.68; Conservative Query Match Best Local Similarity 7; Conserve

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1 ASIAAARVLDY 11

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|: |||| :|| 255 AATAAARAIDY 265

ADS22602 standard; protein; 656 AA

(first entry) 02-DEC-2004

Bacterial polypeptide #11635.

cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide. Recombinant DNA construct; transformed plant; improved plant property;

Bacteria

US2003233675-A1

18-DEC-2003.

20-FEB-2003; 2003US-00369493.

21-FEB-2002; 2002US-0360039P.

(CAOY/)

CAO Y. HINKLE G J. SLATER S C. CHEN X. (HINK/)

GOLDMAN B S. (CHEN/) Goldman BS; Chen X, Hinkle GJ, Slater SC, Cao Y,

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 11635; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a rarnsformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with

improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to harbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html

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Sequence 656 AA;

Gaps ö 72.0%; Score 36; DB 8; Length 656; 63.6%; Pred. No. 1.7e+02; ive 2; Mismatches 2; Indels Query Match 72.0 Best Local Similarity 63.6 Matches 7; Conservative

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1 ASIAAARVLDY 11

255 AATAAARAIDY 265

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RESULT

ABB48560 standard; protein; 708 AA.

ABB48560;

05-FEB-2002 (first entry)

Listeria monocytogenes protein #1264

Antibacterial, gene therapy, vaccine, biosynthesis, biodegradation, vitamin B12; bacterial infection, disease.

Listeria monocytogenes.

WO200177335-A2

18-OCT-2001

11-APR-2001; 2001WO-FR001118.

11-APR-2000; 2000FR-00004629.

(INSP) INST PASTEUR

Dehoux P; Cossart P; C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; O, Checouni F, Nedjari H, Glaser P, Kunst F, Cossart E Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Y T, Domann E, Hain T, Berche P, Charbit A, Durant L; J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; J, De Pablos B, Wehland J, Kaeret U, Entian K, Hauf J; Chakraborty T, Domann E, Perez-Diaz J, Baquero F, Maduenio E, De Pablos B, Rose M, Voss H; Dominguez-Bernal G, Sussurget O, Buchrieser Daniels J,

WPI; 2002-010914/01.

Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.

Claim 6; SEQ ID NO 1265; 192pp; French.

The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins

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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
22-JUN-1999;
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27-JUL-1999;
27-JUL-1999;
  18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
28-MAY-1999;
01-JUN-1999;
                                                                                03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
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30-JUN-1999;
01-JUL-1999;
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16-JUN-1
16-JUN-1
17-JUN-1
18-JUN-1
                                                                                                                    10-JUN-1
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18-JUN-1
18-JUN-1
    expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially blosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                       Gaps
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                                                                                                                                   Score 35; DB 5; Length 708;
Pred. No. 2.9e+02;
                                                                                                                                                      0; Indels
                                                                                                                            70.0%; Score 75.0%; Pred. No. 2... 2; Mismatches
                                                                                                                                                                                                                                                                                       Zea mays protein fragment SEQ ID NO: 19948.
                                                                                                                                                                                                                                    AAG18510 standard; protein; 157 AA
                                                                                                                                                                                                                                                                                                                                                                                                               99US-0121825P
99US-0123180P
99US-0125784BP
99US-0126264P
99US-0126264P
99US-0126234P
99US-0128234P
99US-012845P
99US-013845P
99US-013845P
99US-013845P
99US-0130449P
99US-0130449P
99US-0130449P
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9905-0132487P
9905-0132863P
9905-0134218P
9905-0134218P
9905-013421P
9905-013431P
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                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                      17-OCT-2000 (first entry)
                                                                                                                           Query Match
Best Local Similarity 75.v
Local 6; Conservative
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697 AAARIIDY 704
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                                                                                                                                                                       4 AAARVLDY 11
                                                                                                                    Sequence 708 AA;
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25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
10-APR-1999;
11-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
11-MAY-1999;
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AAG18510
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990S-0134768P.
990S-0134941P.
990S-0135324P.
990S-0135324P.
990S-0136392P.
990S-0136392P.
990S-0136392P.
990S-0137522P.
990S-0137522P.
990S-0137522P.
990S-0137522P.
990S-0139453P.
990S-0139453P.
990S-0139453P.
990S-0139453P.
990S-0139453P.
990S-0139453P.
990S-0139453P.
990S-0139453P.
990S-0140334P.
990S-0140354P.
990S-0140354P.
990S-0140354P.
990S-0140354P.
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990S-0144085P.
990S-0144333P.
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990S-0144333P.
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990S-0144333P.
990S-0144332P.
990S-0144332P.
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990S-0144332P.

1999; 1999; 1999; 1999; 1999; 1999;

1999

990S-0145145P. 990S-0145218P. 990S-014524P. 990S-0145276P. 990S-0145913P.

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990S-0145919P

990S-014638EP

990S-014638BP

990S-0147302P

990S-0147302P

990S-0147303P

990S-0147303P

990S-0147303P

990S-0147303P

990S-0147303P

990S-0147303P

990S-0147303P

990S-0148684P

990S-015080P

990S-015080P

990S-015139P

990S-015139P

990S-015139P

990S-015468P

990S-015403P

990S-015403P

990S-015403P

990S-015403P

990S-015403P

990S-015403P

990S-015403P

990S-015403P

990S-015403P

990S-015659EP

990S-015659EP

990S-015659EP

990S-015659EP

990S-0159331P

990S-0159331P

990S-0169331P

990S-0169331P

990S-016938P

990S-016938P

990S-01698P

990S-016098P

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990S-016098P
27-JUL-1999

28-JUL-1999

28-JUL-1999

02-AUG-1999

03-AUG-1999

04-AUG-1999

04-AUG-1999

05-AUG-1999

06-AUG-1999

06-AUG-1999

11-AUG-1999

12-AUG-1999

13-AUG-1999

13-AUG-1999

13-AUG-1999

13-AUG-1999

13-AUG-1999

14-AUG-1999

15-SEP-1999

16-SEP-1999

16-SEP-1999

17-AUG-1999

18-AUG-1999

19-AUG-1999

19-AUG-1999

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19-AUG-1999

11-AUG-1999

11-AU
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25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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                                                                                                                                                                          Length 157;
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                                                                                                                                                                        DB .
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                                                                                                                                                                          68.0%; Score 34; DB
ilarity 100.0%; Pred. No. 90;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        AAG18509 standard; protein; 159 AA
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990S-0123180P.
990S-012548P.
990S-012548P.
990S-0126264P.
990S-0126782P.
990S-0128234P.
990S-0128434P.
990S-0130449P.
990S-0130449P.
990S-0130449P.
990S-0131449P.
990S-0131449P.
990S-0132488P.
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990S-013488P.
990S-013488P.
990S-013488P.
99US-0161359P.
99US-016136DP.
99US-016132DP.
99US-0161920P.
99US-0161993P.
99US-0161933P.
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                                                                                                                                                                                                                                                                                                          117 AARVLDY 123
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                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
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25-MAY-1999;
27-MAY-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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28 - MAY - 1999; 99US - 0136782P. 03 - UMN - 1999; 99US - 013722P. 04 - UMN - 1999; 99US - 013722P. 06 - UMN - 1999; 99US - 013722P. 08 - UMN - 1999; 99US - 013724P. 08 - UMN - 1999; 99US - 0138644P. 16 - UMN - 1999; 99US - 0138447P. 16 - UMN - 1999; 99US - 0138448P. 18 - UMN - 1999; 99US - 014333P. 19 - UML - 1999; 99US - 0144333P. 22 - UML - 1999; 99US - 0144333P. 23 - UML - 1999; 99US - 0144333P. 24 - UML - 1999; 99US - 0144333P. 25 - UML - 1999; 99US - 0144333P. 27 - UML - 1999; 99US - 0144632P. 23 - UML - 1999; 99US - 0144632P. 24 - UML - 1999; 99US - 0144632P. 25 - UML - 1999; 99US - 0144632P. 27 - UML - 1999; 99US - 0144632P. 28 - UML - 1999; 99US - 014463P. 29 - UML - 1999; 99US - 014463P. 21 - UML - 1999; 99US - 014463P. 22 - UML - 1999; 99US - 014463P. 23 - UML - 1999; 99US - 014463P. 24 - UML - 1999; 99US - 014463P. 25 - UML - 1999; 99US - 014463P. 26 - UML - 1999; 99US - 014463P. 27 - UML - 1999; 99US - 014463P. 28 - UML - 1999; 99US - 01463P. 29 - UML - 1999; 99US - 01463P. 20 - UML - 1999; 99US - 01463P. 21 - UML - 1999; 99US - 01463P. 22 - UML - 1999; 99US - 01463P. 23 - UML - 1999; 99US - 01463P. 2			
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                              Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; of drought tolerance; berblidde; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomanna; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                       Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                  20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                         21-FEB-2002; 2002US-0360039P.
                                                       Bacterial polypeptide #17091
                                 02-DEC-2004 (first entry)
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HINKLE G J.
SLATER S C.
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            ADS28058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY36754-Y37949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antiennes and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, sapingitis, perhappatitis, bartholinitis; pneumopathy in breast feeding infants; and veneraal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases
                                                                                                                                                                                                                                               paratrachoma, inclusion conjunctivitis, genital disease, perihepatitis, nongonococcal uretritis, epidymitis, cervicitis, salpingitis, bartholinitis, pneumopathy, venereal lymphogranulomatosis.
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                                  Gaps
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           Length 159;
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Pred. No. 1e+02;
                                  0; Indels
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                                                                                                                                                                                                               Amino acid sequence of a Chlamydia trachomatis protein.
           DB 3;
91;
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                                  Mismatches
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           Score 34;
Pred. No.
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                                                                                                                                        AAY37904 standard; protein; 180 AA
 68.0%; Scc.
100.0%; Pre
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97FR-00016034.
98US-0107077P.
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77.8%;
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IAAARSMDY 148
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Goldman BS;

Chen X,

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a crop plant such as maize or soybean. The method of producing a transformed plant cauch as maize or soybean. The method of producing a transformed plant cannot an improved property comprises transforming a plant with the cereombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plants with the recombinant DNA construct is useful for improving plants with the collympostide is useful for improved plant properties.

The recombinant DNA construct is useful for improving plants with the collamore to herbicides, extreme osmotic conditions, pathogens or peats, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
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Pred. No. 1.4e+02;
1; Mismatches 1; Indels
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Claim 1; SEQ ID NO 17091; 122pp; English.
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ADS28058 standard; protein; 231 AA.

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RESULT 13 ADS28058

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                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 22440.
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9905-0123180P

9905-012548P

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25-MAR-1999;
29-MAR-1999;
10-APR-1999;
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                                                                                                                                                  AAG20306;
                                                                           RESULT 14
                                                                                              AAG20306
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                         Arabidopsis thaliana protein fragment SEQ ID NO: 65899.
                                                                                                                                                         99US-0121825P

99US-0123180P

99US-012548BP

99US-012664P

99US-0126748BP

99US-0126748PP

99US-0128234P

99US-0128244PP

99US-012844PP

99US-0130891P

99US-0130891P

99US-0132448PP

99US-0132448PP

99US-013248PP

99US-0134941PP

99US-0134941PP

99US-013552PP

99US-013552PP

99US-013552PP

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99US-013552PP

99US-0137724PP

99US-0139453PP

99US-0139455PP
                                                                                                                                          25-FEB-2000; 2000EP-00301439
                         18-OCT-2000 (first entry)
                                                                                         Arabidopsis thaliana
                                                                                                         EP1033405-A2
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16-JUN-1999;
16-JUN-1999;
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18-JUN-1999;
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           AAG51887;
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-MAY-19
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Pred. No. 1.4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100.0%; Por 7; Conservative 0;
990S-0149175P.
990S-0149426P.
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990S-0149929P.
990S-0149929P.
990S-0149920P.
990S-015066P.
990S-015106P.
990S-015106P.
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13-0CT-1999;
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14-0CT-1999;
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-OCT-1999;
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Best Local S:
Matches 7
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99US-0139459P. 99US-0139460P. 99US-0139461P.

18-JUN-1999; 18-JUN-1999; 18-JUN-1999;

AAG51887 standard; protein; 237 AA.

RESULT 15 AAG51887 ID AAG518

AARVLDY 11

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RR 18 - JUN-1999; 99US-0139462P

RR 18 - JUN-1999; 99US-0139750P

RR 21 - JUN-1999; 99US-0139750P

RR 22 - JUN-1999; 99US-0139763P

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RR 22 - JUN-1999; 99US-0139776P

RR 22 - JUN-1999; 99US-0140655P

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RR 22 - JUL-1999; 99US-014331P

RR 22 - JUL-1999; 99US-014331P

RR 23 - JUL-1999; 99US-014331P

RR 24 - JUL-1999; 99US-014331P

RR 24 - JUL-1999; 99US-014331P

RR 25 - JUL-1999; 99US-014331P

RR 05 - JUL-1999; 99US-014331P

RR 05 - JUL-1999; 99US-014331P

RR 05 - JUL-1999; 99US-014331P

RR 12 - JUL-1999; 99US-014331P

RR 14 - JUL-1999; 99US-014332P

RR 14 - JUL-1999; 99US-014332
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PR 27-AUG-1999; 9918-01506RP
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PR 21-SEP-1999; 9918-01560PP
PR 21-SEP-1999; 9
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UD B AAKVLDY 14 Search completed: October 14, 2005, 16:12:40 Job time: 85.5625 secs

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Gaps

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
               Copyright
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- protein search, using sw model OM protein Run on:

October 14, 2005, 16:02:59 ; Search time 15.2969 Seconds (without alignments) 69.190 Million cell updates/sec

US-10-614-959-12 50 Title: Perfect score:

1 ASIAAARVLDY 11 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 8 0 0 0 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	AF2984 3-methylcrotonyl-C			S56849 probable membrane		D87715 carboxymethylenebu		I40371 methyltransferase				DNA polym		conserved	hypothetical	hypothetical		hypothetical	cobyrinic		glutamyl-	S45053 membrane protein	T27970 hypothetical prote			G69502 histidinol-phospha		0.000
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	Query Match Length	663	709	143	692	969	231	279	579	649	926	162	202	202	220	264	358	367	397	441	482	509	614	1027	1232	305	342	363	300
de	Query Match	72.0	72.0	70.0	70.0	70.0	68.0	68.0	68.0	68.0	68.0	99	0.99	99	99	0.99	99	99	0.99	0.99	0.99	0.99	0.99	0.99	99	64.0	64.0	4	· ·
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ALIGNMENTS

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-methylcrotonyl-CoA carboxylase alpha subunit [imported] - Agrobacterium tumefaciens (s

C;Species: Agrobacterium tumefaciens
C;Date: 11.-Jan-2002 #sequence_revision 11.-Jan-2002 #text_change 09-Jul-2004
C;Date: 11.-Jan-2002 #sequence_revision 11.-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2984
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2117-2233, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W. A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AF2984
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-663 <kUR>
A;Cross-references: UNIPROT:Q8UA95; GB:AE008689; PIDN:AAL44292.1; PID:g17741880; GSPDB:GA;Experimental source: strain C58 (Dupont)

A; Gene: mccA C, Genetics

A;Map position: linear chromosome C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy

Gaps .; 0 Length 663; 2; Indels Query Match 72.0%; Score 36; DB 2; Best Local Similarity 63.6%; Pred. No. 27; Matches 7; Conservative 2; Mismatches 2

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1 ASIAAARVLDY 11 ð

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RESULT 2

3-methylcrotonyl-CoA carboxylase alpha chain (AF310338) [imported] - Agrobacterium tumef C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C; Accession. 489829 R; Goddner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Liu, E.; Monlam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Litle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-709 <KUR>

A; Cross-references: UNIPROT: Q8UA95; GB: AE007870; PIDN: AAX89915.1; PID: g15159866; GSPDB: G

A; Gene: AGR L 2704

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Best Local Similarity 70.0
Matches 7; Conservative
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nes 6; Conservative
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685 AAARIIDY 692
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               A; Accession: S47117
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A,Accession: $50798
A,Accession: $50798
A,Status: nucleic acid sequence not shown; translation not shown
A,Residues: 135-692 «VAN»
A,Residues: 135-692 «VAN»
A,Residues: 135-692 «VAN»
A,Residues: 135-692 «DIN»
A,R
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N.Alternate names: hypothetical protein HRC558; hypothetical protein J1083
N.Alternate names: hypothetical protein HRC558; hypothetical protein J1083
C.Species: Saccharomyces cervisiae
C.Species: Saccharomyces
C.
A,Map position: linear chromosome
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                     Score 36; DB 2; Length 709;
Pred. No. 29;
2; Mismatches 2; Indels
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A,Accession: S56847
A,Molecule type: DNA
A,Residues: 115-692 < POH>
A,Crose-references: EMBL:Z49348; MIPS:VJL073w
R,Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, Yeast 11, 57-60, 1995
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                                                                                                                                                                                                                             Query Match 72.0%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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Matches 8; Conservative
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7 ASLAAARVL 15
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- Listeria monocytogenes
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C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
R.Gacession: B. M.; Bearth 1.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L. M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Atterence number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1210
A;Status: preliminary
A;Alcatus: preliminary
A;Alcatus: Johannary
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: D87715
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11229647
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A;Cross-references: UNIPROT:Q8Y833; GB:NC_003210; PIDN:CAC99163.1; PID:g16410487; GSPDB
A;Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.0%; Score 35; DB 2; Length 692; 70.0%; Pred. No. 45; 1; Indels rative 2; Mismatches 1; Indels
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A;Residues: 1-692 <SOR>
A;Cross-references: EMBL:X88851; NID:g895892; PID:g895898
A;Molecule type: DNA
A;Residuse: 135-692 <VAM>
A;Cross-references: EMBL:Z34288; NID:g498992; PID:g498993
R;Sor, F.J.
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F;585-655/Domain: dnaJ amino-terminal homology <DNJ>
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A;Map position: 10L
C;Keywords: transmembrane protein
                                                                                                                                                    submitted to the EMBL Data Library, June 1995
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hypotherical protein SPAC443.03c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: 138883
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EWBL Data Library, February 1996
A;Reference number: 221807
A;Accession: T3888
A;Accession: T38
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C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Date: 13.-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C; Accession: B71468
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 734-759, 1998
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac: A; Reference number: A71570; MUID:99000809; PMID:9784136
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A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF1059
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connetton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;tile: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
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C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4H3.03c
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631 AAIAAAHILD 640
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IAAARSMDY 924
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les 7; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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C;Genetics:
A;Gene: becCIM
C;Superfamily: site-specific methyltransferase (adenine-encoific) h.c...
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FEBS Lett. 183, 195-200, 1985
A;Title: Complete primary structure of thermitase from Thermoactinomyces vulgaris and it
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C,Genetics:
A;Gene: CC3758
C;Superfamily: carboxymethylenebutenolidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1-279 < MEL.
A; Cross-references: UNIPROT: P04072
C; Comment: This protein is enzymatically similar to a proteinase from Streptomyces sp. C; Superfamily: subtilisin; subtilisin homology
C; Scwoords: Hydrolase; serine proteinase
F; 29-239/Domain: subtilisin homology < SBF.
F; 38,71,225/Active site: Asp, His, Ser #status predicted
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C;Species: Thermoactinomyces vulgaris
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A00973
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Pred. No. 28;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                         Length 231;
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methyltransferase - Bacillus stearothermophilus (fragment)
                                                                                                                                                                                                                                                     Match 68.0%; Score 34; DB 2; Local Similarity 80.0%; Pred. No. 23; Les 8; Conservative 1; Mismatches 1
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ilarity 80.0%;
Conservative
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26 AEVIAKRILDY 36
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96 ASILAVRVLD 105
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Best Local Similarity
Matches 6; Conserv?
A; Molecule type: DNA
A; Residues: 1-231 <STO>
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Conserved hypothetical protein SA0939 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Obla; T.; Colayana, T.; Colayana, M.; Colayana, M.; Colayana, M.; Colayana, M.; Colayana, T.; Colayana, M.; Colayana, T.; Colayana, M.; Colayana, T.; Colayana, M.; 
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A; Experimental source: strain N315
A; Genetics: A,Genetics: A
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A,Experimental source: strain Delta H
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A;Molecule type: DNA
A;Residues: 1-264 <MTH>
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Best Local Similarity 54.5
Matches 6; Conservative
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94 ASIAAVKLINY 104
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131 NVASASVLDY 140
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           1 ASIAAARVL 9
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: By7609
A;Status: preliminary
A;Wolecule type: DNA
A;Residues: 1-202 <KUR>
A;Cross-references: UNIPROT:Q8UDP4; GB:AE007869; PIDN:AAK87827.1; PID:g15157207; GSPDB:GC;Genetics:
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Crossi-teferences: UNIPROT:Q8UDP4; GB:AE008688; PIDN:AAL43068.1; PID:g17740536; GSPDB:GA;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable DNA polymerase III, epsilon chain [imported] - Agrobacterium tumefaciens (strai
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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A; Molecule type: DNA
A; Residues: 1-162 <PAR>
A; Cross-references: GB: AL513382; PIDN: CAD06923.1; PID: g16505571; GSPDB: GN00176
C; Genetics:
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Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
Accession: B97609
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A;Map position: circular chromosome
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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112 AVARILDY 119
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A;Gene: STY4801
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GenCore version 5.1.6
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OM protein - protein search, using sw model	October 14, 2005, 15:51:44; Search time 73.2188 Seconds (without alignments) 76.932 Million cell updates/sec
OM protein	Run on:

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

מעולה זכיים למעולה

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	1	Q8efs2 shewanella	Q882e4 oryza sativ	Q8gu81 oryza sativ	Q62cx8 burkholderi		Q8ua95 agrobacteri			Q7ma36 wolinella s	Q69x93 oryza sativ	•	Q6aq91 desulfotale	Q9rjr7 streptomyce				Q7r034 giardia lam	Q6na42 rhodopseudo	Q9a213 caulobacter					Q91805 arabidopsis	Q9fv51 arabidopsis	Q8p714 xanthomonas			Q9rgk2 bacillus st	Q7f1d1 oryza sativ
	ID	Q6H820	Q8EFS2	Q8S2E4	Q8GU81	Q62CX8	Q63M18	Q8UA95	Q7CSK5	Q8H034	Q7MA36	Q69X93	Q69582	Q6AQ91	Q9RJR7	YJH3 YEAST	Q8Y8 <u>3</u> 3	Q6MK31	Q7R034	Q6NA42	Q9A213	THET_THEVU	Q6AH23	Q8ZSL1	Q8ZXL8	Q9LS05	Q9FV51	Q8P7L4	Q8PIY6	MTC1_BACST	Q9RQK2	Q7F1D1
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A. C.	Match	74.0	74.0	74.0	74.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0
	Score	37	37	37	37	36	36	36	36	36	36	36	35	35	35	35	35	35	35	34	34	34	34	34	34	34	34	34	34	34	34	34
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OlyMAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Acetyl-CoA carboxylase, biotin carboxylase, putative.
OrderedLocusNames=SO1894;
Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Shewanellaceae; Shewanella.

694 AA.

PRT;

PRELIMINARY;

QBEFS2 QBEFS2;

RESULT 2 Q8EFS2 [1] — SEQUENCE FROM N.A. SERAIN-RR-1; MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

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Q7qh89 Q10211 Q65g00 Q67g00 Q67r60 Q8xwi9 Q8xwi9 Q8xp1 Q8xxp1 Q8xxp1 Q8xxp1 Q8xxp1 Q8xxp1				,	a, Tracheophyta; Poaceae;		ses.			gth 421; Indels			
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Q7QH89 VAX3 CAY3 CAX3 Q6FY30 Q6FY30 Q67R60 Q67R60 Q7R273 Q8ZXP1 Q	AL1		PRT;	TrEMBLrel. 27, Created) TrEMBLrel. 27, Last seque (TrEMBLrel. 27, Last anno N.acetyltransferase-like	Name=COLZOT_COS-7_COS-7 Oryza astiva (japonica cultivar-group). Eukaryota, Viridiplantae, Streptophyta, Embryophy Spermatophyta, Magnoliophyta, Liliopsida, Poales, Enrhartoideae, Oryzeae, Oryza.	OM N.A. Matsumoto T., Yamamoto K.;	001) to the EMBL/GenBank/DDBJ d BAD2s129.1; F:N-acetyltransferase activity; F:transferase activity; IEA. 1182; GCNSacetyl trans.	InterPro; IPR000504; RNA_rec mot. Pfam, PF00583; Acetyltransf 1; 1. PROSITE; PS00030; RRM_RNP 1; UNKNOWN	7A5	88			
				, Light	ultiva ; Stre phyta; Oryza.	aman	e Ey trar ase cety	1,1,1	MW;				
				27, 27, 27, ansf	cul phy Or	Υ.	tyl fer NSa	RNA_rec transf_ RNP_1;	44979 MW;	74.0%; 80.0%; ive			
596 649 8824 866 874 912 920 945 162 162 162			PRELIMINARY	rel. rel. rel. yltr	1.4; aponica c diplantae Magnoliop Oryzeae;	H	25129 25129 -acet ransf	04; RN etyltr RRM_R	449	74. larity 80. Conservative	10	297	
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		п	Q6H820 Q6H820	05-JUL-2004 (05-JUL-2004 (05-JUL-2004 (GCN5-related	Name=0J1297 C09.4 Oryza gativa (jap Eukaryota, Viridi Spermatophyta; Ma Ehrhartoideae; Or NCBI_TaxID=39947;	[1] SEQUENCE FROM N.A. Sasaki T., Matsumoto	Submitted (AUG-2001) to the RMBL; APO04087; BAD25129.1; GQ; GQ:0008080; F:N-acetylt GQ; GO:0016740; F:transfera InterPro; IPR000182; GGNSac	InterPro; IPR0005 Pfam; PF00583; Ac PROSITE; PS00030;	Iransierase SEQUENCE	Loca			
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ATP-binding
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., A Read T.D., Eisen J.A., Seehadri R., Ward N.L., Methe B.A., Clayron R.A., Meyer T. Tsapin A., Soatd N.L., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., A Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., Mite O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M., Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J., Leterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Vorter J.C., Nealson K.H., Fraser C.M.; transfer Genome sequence of the dissimilatory metal ion-reducing bacterium T. Shewanella oneidensis.";

I. Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
PubMed=1244438; DOI=10.1038/nature01184;
Sasaki T., Matsumcto T., Yanmanoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
Karasawa W., Katagiri S., Kikuta A., Kobayashi T., Mukai Y.,
Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
Magasaki H., Nakashima M., Nakamachi Y., Nakamura M.,
Nagasaki H., Nakashima M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
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Name=P0022E10.15;
Norza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.0%; Score 37; DB 2; Length 694; 54.5%; Pred. No. 1.1e+02; ive 4; Mismatches 1; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                               InterPro; IPR001882; Blotin BS.
InterPro; IPR001882; Blotin Carb C.
InterPro; IPR001893; Blotin Carb C.
InterPro; IPR005481; Blotin lipoyl.
InterPro; IPR005491; Cphp Synth L D2.
InterPro; IPR01053; Hybrid motif.
InterPro; IPR011053; Hybrid motif.
Pfam; PF02785; Blotin carb C; 1.
Pfam; PF00289; CPSase L chain; 1.
Pfam; PF00289; CPSase L chain; 1.
                                                                                                                                                                                                                                      GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:bictin binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:000152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00866; CPSASE 1; UNKNOWN 1.
PROSITE; PS00867; CPSASE 2; UNKNOWN 1.
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268 AAVAAKAIDY 278
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Best Local Similarity
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TIGR; SO1894;
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Q8S2E4
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GO; GO: 0016021; C:integral to membrane; IEA.

RG; GO: 0016021; C:integral to membrane; IEA.

RG; GO: 0016021; E:ATP binding; IEA.

RG; GO: 0016026; F:ATP ase activity, coupled to transmembrane m. . .; IEA.

RG; GO: 001616; F:uncleotide binding; IEA.

RG; GO: 0006810; P:transport; IEA.

RG; GO: 0006810; P:transport; IEA.

RITERPO: IPR011527; ABC_membrane.

RITERPO: IPR01140; ABC_TRNSporter.

RR; FFG; FFG; FFG; FFG; FFG; FFG;

RR; FFG; FFG; FFG; FFG; FFG; FFG;

RR; FFG; FFG; FFG; FFG; FFG; FFG;

RR; SR0021; ABC_transporter; 2.

RRGITE; PS50929; ABC_TRNSPORTER.1; 2.

RRSITE; PS50893; ABC_TRANSPORTER.2; 2.
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GO: 00005524; F:ATP binding; IEA.
GO: 00005524; F:ATP binding; IEA.
GO: 00001665; F:ATPase activity, coupled to transmembrane m. . .; IEA.
GO: 0000166; F:Nucleotide binding; IEA.
GO: 0000166; F:Nucleotide binding; IEA.
InterPro: IPR001539; AAA ATPase.
InterPro: IPR001527; ABC membrane 1.
InterPro: IPR001140; ABC_IM_transpt.
Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Yano M., Jiang J., Gojobori T., imithe genome sequence and structure of rice chromosome 1.";
Nature 420:312-316(2002).
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TAXID=39947;
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-i- SINTLARITY: Belongs to the ABC transporter family.
EMBL; AJ535055; CAD59577.1; -.
HSSP; P08716; 1MT0.
                                                                                                                                                           -i- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AP003229; BAB89499.1; -.
HSSP; P08716; 1MT0.
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1-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MDR-like ABC transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.0%; Score 37; DB 2; I
70.0%; Pred. No. 1.9e+02;
ive 2; Mismatches 1;
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Length 402; 0, Indels

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PubMed=1537794;
A Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Bencles T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
Reltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
R. Reith K.E., Maddison M., Moule S., Price C., Quail M.A.,
Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
Songalvial S., Stewans K., Tunapa S., Vesaratchaves M.,
Mhitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
"Genomic plasticity of the causative agent of melioidosis,
Burkholderia pseudomallei.";
Burkholderia pseudomallei.";
Broc. Nall. Acad. Sci. U.S.A. 101:14240-14245(2004).
REBL; BX5/1966; CAH33304.1; -.
SEQUENCE 402 AA, 41596 MW; 6FCA16BE0F4B18EA CRC64;
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"The genome of the natural genetic engineer Agrobacterium tumefaciens
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
3-methylcrotonyl-CoA carboxylase alpha subunit.
Name=mcCA; OrderedLocusNames=Atu3479;
Sagobacterium tumefaciens (Strain CS8 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobiaceae; Rhizobiacterium group; Agrobacterium.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016874; F:Ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
PÉam; PF00785; Biotin carb C; 1.
Pfam; PF00184; Biotin lipoyl; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00866; CPSASE 1; UNKNOWN 1.
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ERBEL, ARG09278; AAL44292.1; -.
PIR, A98299; A98299.
PIR, AF2984; AF2984.
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Best Local Similarity 70...
7; Conservative
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Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
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Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
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Zhou L., Fraser C.M.;
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Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).

EMBL; CP000011; AAU46877.1; -
SEQUENCE 402 AA, 41596 MW, 6FCA16BE0F4B1BEA CRC64;
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Putative transporter protein.
ORFNames=BPSS0842;
Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiaceae; Burkholderia.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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Pred. No. 2e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                   1234 AA; 134571 MW; C5F9E9D75D28AC93 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Major facilitator superfamily protein.
ORFNames=BMAA0712;
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InterPro; IPR003439; ABC_transporter.
Pfam; PF00664; ABC_membrane; 2.
Probom; PF000005; ABC_tran; 2.
Probom; PP0000006; ABC_transporter; 2.
SMART; SM0382; AAA; 2.
PROSITE; PS50929; ABC_TMIF; 2.
PROSITE; PS50921; ABC_TRANSPORTER_1; 2.
PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
ATP-binding.
SEQUENCE 1234 AA; 134571 MW; C5F9B9D75
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70.0%;
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Best Local Similarity 70.0.
Local Similarity 70.0.
Ti Conservative
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Best Local Similarity 70...
7; Conservative
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106 ATVAAARLLD 115
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RESULT 5
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100 062CX8
100 062C
DT 25-0
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Q63M18; Q63M18

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RESULT 6
063M18
10 063M 
AC 063M 
DT 25-00
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Hypothetical protein OJ1172F09.9.
Name=OJ1172F09.9;
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MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2321-2328 (2001).
EMBL, AE008334; AA889915.1; -.
HSSP: P02905; 1BDO.
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Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Batteria, Proteobacteria, Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=176299;
  Score 36; DB 2; Length 663;
Pred. No. 1.7e+02;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                 2; Mismatches
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InterPro; IRR005482; Biotin Garb C.
InterPro; IRR005482; Biotin Larb C.
InterPro; IRR005481; CPase L N.
InterPro; IRR005479; Cphp synth L D2.
InterPro; IRR01053; Wybrid motif.
InterPro; IRR011053; Wybrid motif.
Ffam; PF002785; Biotin carb C; I.
Ffam; PF00364; Biotin lipoyl; I.
Ffam; PF00364; Biotin lipoyl; I.
Fram; PF00369; CPSase L chain; I.
FROSITE; PS00188; BIOTIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:bictin binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
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PROSITE; PS00867; CPSASE 2; UNKNOWN 1
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    72.0%;
63.6%;
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Query Match 72.0
Best Local Similarity 63.6
Matches 7; Conservative
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Matches 7; Conservative
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258 AATAAARAIDY 268
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304 AATAAARAIDY 314
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                                                                                             1 ASIAAARVLDY 11
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Q8H034
ID Q8H0:
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MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
Mandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
Meyer F., Lederer H., Schuster S.C.;
"Complete genome sequence and analysis of Wolinella succinogenes.";
Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
EMBL, BX574658; CAE096281. -
GO; GO:0019861; C.flagellum; IRA.
InterPro; IPR008940; Prenyl_trans.
InterPro; IPR008940; Prenyl_trans.
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Wolinella.
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
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                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008938; ARM.
Hypothetical protein.
SEQUENCE 723 AA; 78613 MW; 3FD842215E6ED1FD CRC64;
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PROSITE; PS50293; TPR REGION; 1.
Complete protecome; Flagellum.
SEQUENCE 778 AA; 89775 MW; 382P992CE949C27E CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
FLAGELLAR FUNCTIONAL PROTEIN.
Name-PFLA, OrderedLocusNames=WS0490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.0%; Score 36; DB 2; I
80.0%; Pred. No. 1.9e+02;
iive 1; Mismatches 1;
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Pred. No. 2e+02;
2; Mismatches
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63.6%;
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Best Local Similarity 63.6
Matches 7; Conservative
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Les 8; Conservative
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616 ASLAAARVTD 625
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                                                                                                                          NCBI_TaxID=39947;
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Gaps

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STRAIN=LSV54 / DSM 12343;
PubMedc15305914;
Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
Klenk H.-P.,
"The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
from permannently cold Arctic sediments.";
EMBL; CR522870; CAG35482.1; -.
"A transforming fragment within the direct repeat region of human herpesvirus type 6 that transactivates {\rm HIV-1."}_i, Oncogene 9:1167-1175(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desulfotalea psychrophila.
Bacteria, Proteobacteria, Deltaproteobacteria, Desulfobacterales,
Desulfobulbaceae, Desulfotalea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
Bacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%; Score 35; DB 2; Length 184; 80.0%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                               Length 143;
                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                Thompson J.T.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; X33675; CRA52028.1; -.
PIR; 543071, 843071.
SEQUENCE 143 AA; 13317 MW; EDF78898C3D31734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 AA; 20792 MW; 8D9DCB5EDFAA60AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                            Score 35; DB 2;
Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 AA.
                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
Putative zinc-binding oxidoreductase.
ORFNames=SCF51.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                            70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 86.5.
Ref. Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=DP0753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 80.0
nes 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 AAIAAARVIN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ASIAAARVLD 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 ASLAAARVL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ASIAAARVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2) / M145;
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=84980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6AQ91
Q6AQ91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RJR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9RJR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6AQ91
         SCREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                              Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
BEDLINE-24181269; PubMed=8134119;
Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z., Frenkel N., Rosenthal L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO:0005524; F.ATP binding; IEA.
GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO:0004713; F:protein-tyrosline kinase activity; IEA.
GO:0004872; F:receptor activity; IEA.
GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family EMBL; AP003622; BAD32908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.0%; Score 36; DB 2; Length 1072; 80.0%; Pred. No. 2.7e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1072 AA; 114368 MW; E15B809971B15F78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humān herpesvīrus 6.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative receptor-like protein kinase 2.
Name=P0633E08.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Herpesvirus Type 6 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0019; LEURICHRPT.

Prodom; PD000001; Prot kinase; 1.

SMART; SM00369; LRE TF; 11.

SMART; SM00219; TYTKC; 1.

SMART; SM00219; TYTKC; 1.

PROSITE; PS00101; PROTEIN KINASE ATP; UNKNOWN 1.

PROSITE; PS00119; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.
   PRT; 1072 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001611; IRR.
InterPro; IPR007090; IRR plant.
InterPro; IPR0070391; IRR Lyp.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008270; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR001245; Tyr pkinase.
Fam; PP00560; IRR 1; 22.
Pfam; PP00069; Pkinase: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004872; F:receptor activity of GO:000468; F:protein amino a InterPro; IPR011009; Kinase_like. InterPro; IPR001611; IRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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116 ASLAALRVLD 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR002085; Adh zn. family.
InterPro; IPR011032; GroES_like.
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitsch B., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Shary S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Mature 417.141-147(2002).
EMBL; AL939105; CAB59716.1; -.
HSSP; Q8L3C8; 11XZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FBB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 34, Last annotation update)
Mypochetical 80.4 kDa protein in SMC3-MRPL8 intergenic region.
OrderedLocusNames=VJL073W; ORFNames=J1083, HRC558;
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycetina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.0%; Score 35; DB 2; Length 329; 70.0%; Pred. No. 1.4e+02; rive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sor F.J.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Entian K.D.;
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 AA; 34155 MW; 5DCAD4FB174FD042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           692 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00107; ADH_zinc_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 SLGAAHVLDY 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rose M., Koetter P.,
Submitted (SEP-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S288C;
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P40358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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YJH3_YEAST
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Matches
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EMBL; X88851; CAA61312.1; -.

EMBL; Z34268; CAA64049.1; -.

R EMBL; Z34268; CAA64049.1; -.

R HSP; PO8622; 1BQZ.

R GernOnline; 141687; -.

R GernOnline; 141687; -.

R GO; GO:0003609; JEMI.

GO; GO:0000360; C:peripheral to membrane of membrane fraction; IDA.

GO; GO:0000742; P:co-chaperone activity; IGI.

GO; GO:0000742; P:raryogamy during conjugation with cellular . . .; IGI.

R GO; GO:0000742; P:protein folding; IGI.

R InterPro; IPRO1623; DnaJ. N.

F Fam; PRO0256; DnaJ; 1.

SMART; SM0071; DnaJ; 1.

PROSITE; PS00076; DNAJ_1; FALSE_NEG.

R Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.0%; Score 35; DB 1; Length 692; 70.0%; Pred. No. 2.9e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    692 AA; 80381 MW; 9F612DD16B66981B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Poly-Gln.
                                                                                                                                                                                                                                                                                                                                                                                                                                               J-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 70.0
Matches 7; Conservative
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SLAAAIILDY 254
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Sequence 6, Appli
Sequence 7, Appli
Patent No. 5472855
Sequence 10, Appl
Sequence 10, Appl
Sequence 3417, Appli
Sequence 3417, Appli
Sequence 1164, Appli
Sequence 1164, Appli
Sequence 1164, Appli
Sequence 1164, Appli
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3193, Ap
16309, A
17003, A
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31470, A
10906, A
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Sequence 19, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                     October 14, 2005, 16:00:04; Search time 21.6562 Seconds (without alignments) 37.917 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                   GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-383-667-12

US-09-3483-667-19

US-09-3483-648-2

US-08-865-203-6

US-07-849-420-6

US-09-253-424-6

US-09-115-658-4

US-09-115-658-4

US-09-115-658-4

US-09-115-658-4

US-09-115-658-4

US-09-115-658-4

US-09-115-658-4

US-09-115-658-1

US-09-115-622

US-09-285-6

US-09-286A-10

US-09-289-12051

US-09-289-1347-1003

US-09-252-991A-17003

US-08-252-991A-17003

US-08-252-991A-17003

US-08-252-991A-17003

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US-08-252-991A-17003

US-08-252-991A-17003

US-08-252-991A-17003

US-08-275-762-55
                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                           513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
Sequence:
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38, Appl
55, Appl
38, Appl
38, Appl
38, Appl
55, Appl
55, Appl
45191, A
22574, A
28830, A
22574, A
223711, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/0938367
; Sequence 12, Application US/0938367
; Patent No. 662495
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W. APPLICANT: Baton, Dan L. APPLICANT: Baton, Dan L. APPLICANT: Baton, Dan L. APPLICANT: Hass, Philip E. APPLICANT: Hass, Philip E. APPLICANT: Kirchhofer, Daniel APPLICANT: Kirchhofer, Daniel APPLICANT: Kirchhofer, Daniel APPLICANT: Kirchhofer, Daniel APPLICANT: Begett, Shelley TITLE OF INVENTION: Human Anti-Factor IX/IXA Antibodies TILE REFERENCE: 91661R2
; CURRENT APPLICATION NUMBER: US 60/098,233
; EARLIER APPLICATION NUMBER: US 60/122,767
; MUMBER OF SEQ ID NOS: 32
; SEQ ID NO 12
; LEMOTH: 11
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APPLICANT: Devaux, Brigitte
APPLICANT: Baton, Dan L.
APPLICANT: Hass, Philip B.
APPLICANT: Hass, Philip B.
APPLICANT: Kirchhofer, Daniel
APPLICANT: Suggett, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILB REFERENCE: P1661R2
                          US-09-295-028-38
US-09-296-028-55
US-09-106-582-55
US-09-106-582-55
US-09-159-469-55
US-09-159-469-55
US-09-693-542-55
US-09-693-542-55
US-09-693-542-55
US-09-693-542-55
US-09-252-991A-32574
US-09-252-991A-32574
US-09-252-991A-28830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-27088
US-09-509-902A-11
US-09-489-039A-14332
                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-23711
US-09-902-540-12245
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Patent No. 6624295
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 11; Conservative
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, ORGANISM: Homo sapiens
US-09-383-667-12
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ZIP: 11753

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,203
TITLE OF INVENTION: Endoproteolytic P
TITLE OF INVENTION: Endoproteolytical
TITLE OF INVENTION: Production Of Pro
TITLE OF INVENTION: Production Of Pro
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOFPMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRA.

ZIF: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
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US-07-849-420-6
i. Sequence 6, Application US/07849420
i. Patent No. 5989856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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STRANDEDNESS: si
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Y: U.S.A.
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Sequence 6, Application US/08865203
Setuch No. 5935815
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Marie Wilhelmina
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van Duijnhoven, Johannes Lambertus Petrus
APPLICANT: Robrock, Antonius Johannes Maria
APPLICANT: Robrock, Antonius Johannes Maria
APPLICANT: Robrock, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 3; Length 755; Pred. No. 30;
                                                                                                                                                                                                                                                                Score 46; DB 4; Length 11;
Pred. No. 0.0013;
0; Mismatches 1; Indels
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Affally Joan
APPLICANT: Rafalaki, Antoni
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB-1169-B
CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/02,659
EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Office 97
SEQ ID NO 2.
LENGTH: 755
                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                      CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
LENGTH: 11
        CURRENT APPLICATION NUMBER: US/09/383,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09342648
Patent No. 6248584
GENERAL INFORMATION:
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72.7%;
                                                                                                                                                                                                                                                                  92.0%;
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
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ORGANISM: Zea mays
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LOCATION: (179)
FEATURE:
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US-09-342-648-2
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US-08-865-203-6
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Gaps
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APPLICANT: van de Ven, Willem Jan Marie
APPLICANT: van de Noweland, Anna Maria Wilhelmina
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van den Ouweland, Anna Maria Maria
APPLICANT: Kobroek, Antonius Johannes Maria
APPLICANT: Koning, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytic Activity; A Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Endoproteolytic Activity, A Process for
Endoproteolytically Processing (Precursor)
Proteins And For The (Micro)Biological
Production Of Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/865,203
FILING DATE: 29-MAY-1997
CLASSIFICATION: 424
ATORNEY/AGENI INFORMATION:
NAME: Tran, Jessica H.
REGISTRATION NUMBER: 40,846
REPERBNCE/DOCKET NUMBER: 294-41 DIV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1870RATION:
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LENGTH: 278
TYPE: PRT
ORGANISM: Thermoactinomyces vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08955424
Patent No. 6274365
GENERAL INFORMATION:
                                                                                                                                                                                      68.0%;
         SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                 Query Match
Best Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-253-854-6
                                                                                                                                                                                                                                                                                                                    96 ASILAVRVLD 105
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Endoproteolytically Processing (Precursor)
Proteins And For The (Micro)Biological
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Pred. No. 25;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: van de Ven, Willem Jan Marie;
APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: van Duijnhoven, Johannes Lambertus Petrus;
APPLICANT: Robrock, Antonius Johannes Maria; and
APPLICANT: Roning, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytic Activity; A Process f
TITLE OF INVENTION: Proteins And For The (Micro)Biologica
TITLE OF INVENTION: Production Of Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294-41 DIV II/CON
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/849,420
FILING DATE: 19920624
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: MOCENT, Thomas F.
REGISTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 2805/41413
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION OF 550
TELECOMMUNICATION OF 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 anino acids
TWDE: amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
PILING DATE: Unassigned
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: HOFFMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-253-854-6
; Sequence 6, Application US/09253854
Sequent No. 6132717
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Tran, Jessica H.
REGISTATION NUMBER: 40,846
REERENCE/DOCKET NUMBER: 294-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.0%;
80.0%;
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Best Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-849-420-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 ASILAVRVLD 105
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GENERAL INFORMATION:

JENERAL INFORMATION:

APPLICANT: Van de Ven, Willem Jan Marie

APPLICANT: Van de Ouweland, Anna Maria Wilhelmina

APPLICANT: Van de Ouweland, Anna Maria Wilhelmina

APPLICANT: Van Duijhoven, Johannes Lambertus Petrus

APPLICANT: Koning, Piet Nico Maria

APPLICANT: Roebroek, Antonius Johannes Maria

APPLICANT: Roebroek, Antonius Johannes Maria

TITLE OF INVENTION: PRARMACEUTICAL COMPOSITION HAVING AN ENDOPROTEOLYTIC

TITLE OF INVENTION: PRODUCTION OF PROTEINS

TITLE OF INVENTION NUMBER: 08/568,152

EARLIER APPLICATION NUMBER: 07/849,420

EARLIER PILING DATE: 1992-06-24

EARLIER FILING DATE: 1992-06-24

EARLIER PILING DATE: 1990-10-21

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PARCHILIN VET: 2.0
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in Sequence 4, Application US/09135658

is Sequence 8, S972683

is Patent No. 5972683

is Patent No. 5972683

is Patent No. 5972684

is APPLICANT: TSAI, Ying-Chieh

is APPLICANT: TSAI, Ying-Chieh

is TITLE OF INVENTION: MUTANT TYPE SUBTILISIN YAB AND ITS APPLICATION

is TITLE REFERENCE: 6653-011-999

is CURRENT APPLICATION NUMBER: US/09/135,658

is CURRENT APPLICATION NUMBER: 86112766

is EARLIER PILING DATE: 1997-09-04

is NUMBER OF SEQ ID NOS: 8

is SOFTWARE: PatentIn Ver. 2.0 - beta

is SEQ ID NO 4

is LENGTH: 279
                                                                                  Gaps
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Score 34; DB 3; Length 278;
Pred. No. 25;
0; Mismatches 2; Indels
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68.0%; Score 34; DB 4; Length 279; 80.0%; Pred. No. 25; 2; Indels ive 0; Mismatches 2; Indels
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          Sequence 9, Application US/09196281A

Patent No. 6605458

GENERAL INFORMATION:
APPLICANT: Hanean, Peter K.
APPLICANT: Bauditz, Peter
APPLICANT: Mikelsen, Frank
TITLE OF INVENTION: Protesse Variants And Compositions
FILE REFERENCE: 5435.200-US
CURRENT APPLICATION NUMBER: US/09/196,281A
CURRENT APPLICATION NUMBER: 1332/97
EARLIER APPLICATION NUMBER: 1332/97
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
5472855.6
; Patent No. 5472855
; Patent No. 5472855
; Patent No. 5472855
; TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/287,964
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 90,902
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 39,652
; FILING DATE: 14-JAN-1992
; APPLICATION NUMBER: 33,039
; FILING DATE: 04-APR-1987
; FILING DATE: 04-APR-1987
; FILING DATE: 01-DEC-1987
; APPLICATION NUMBER: 137,134
; FILING DATE: 01-DEC-1987
; APPLICATION NUMBER: 1858,594
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 1858,594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 6;
Pred. No. 25;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-APR-1986
APPLICATION NUMBER: 614,612
FILING DATE: 29-MAY-1984
FILING DATE: 29-MAY-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 614,617
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,491
FILING DATE: 29-MAY-1984
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bacillus
US-09-196-281-9
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    US-09-196-281-9
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                                                          Score 34; DB 2; Length 279;
Pred. No. 25;
0; Mismatches 2; Indels
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Pred. No. 25;
0; Mismatches 2; Indels
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Pred. No. 25;
0; Mismatches 2; Indels
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Patent No. 658938

GENERAL INFORMATION:
APPLICANT: Hansen, Peter
APPLICANT: Mikkelsen, Frank
APPLICANT: Andersen, Kim
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5348.204.US
CURRENT APPLICATION NUMBER: US/09/515,150A

CURRENT APPLICATION NUMBER: 2000-02-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hansen, Peter
APPLICANT: Banditz, Peter
APPLICANT: Banditz, Peter
APPLICANT: Mikkelsen, Frank
APPLICANT: Mikkelsen, Kim
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5349.204-US;
CURRENT APPLICATION UNMBER: US/09/512,251A
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6:
LENGTH: 279
                                                                                                                                                                                                                                                                        US-09-512-251A-6
; Sequence 6, Application US/09512251A
; Patent No. 6555355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.0%;
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80.0%;
                                                            Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
; ORGANISM: Bacillus subtilis US-09-135-658-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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ORGANISM: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-515-150A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-512-251A-6
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LENGTH: 279
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US-09-710-279-622
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                                                                                                                                                   Query Match 66.0%; Score 33; DB 4; Length 85; Best Local Similarity 70.0%; Pred. No. 9.8; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: October 14, 2005, 16:22:01
Job time : 22.6562 secs
                                          NAME/KEY: MISC_PEATURE
) LOCATION: (30)...(33)
) OTHER INFORMATION: Gap in alignment
US-09-698-286A-10
OTHER INFORMATION: Gap in alignment FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 66.0
Best Local Similarity 60.0
Matches 6; Conservative
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71 SIAAGKPLDY 80
                                                                                                                                                                                                                                         2 SIAAARVLDY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SIAAARVLDY 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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Sequence 10, Application US/09698286A

Patent No. 6677442

GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Kentucky Research Foundation
TITLE OF INVENTION: Human REVI Gene and Protein As Diagnostic, Preventive, and Therap FILE REPERENCE: 050229-0247
CURRENT APPLICATION NUMBER: US/09/698,286A
CURRENT APPLICATION NUMBER: 60/162,140
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 85
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ORGANISM: C. elegans, A. thaliana, S. cerevisiae, S. pombe and H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.0%; Score 34; DB 6; Length 279; 80.0%; Pred. No. 25; ive 0; Mismatches 2; Indels
                                                                                                                      TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
NUMBER OF SEQUENCES: 31
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,964
FILING DATE: 22-SEP-1994
FILING DATE: 12-SEP-1994
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: 90,902
FILING DATE: 14-JAN-1992
APPLICATION NUMBER: 90,902
FILING DATE: 14-JAN-1992
APPLICATION NUMBER: 35,652
FILING DATE: 06-APR-1987
APPLICATION NUMBER: 35,652
FILING DATE: 10-DC-1987
APPLICATION NUMBER: 35,652
FILING DATE: 01-DC-1987
APPLICATION NUMBER: 36,657
FILING DATE: 01-DC-1987
APPLICATION NUMBER: 846,627
FILING DATE: 01-DC-1986
APPLICATION NUMBER: 86,594
FILING DATE: 30-APR-1986
APPLICATION NUMBER: 614,612
FILING DATE: 30-APR-1986
APPLICATION NUMBER: 614,615
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,615
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,617
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,617
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,617
FILING DATE: 29-MAY-1984
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NAME/KEY: MISC_FEATURE
LOCATION: (17)...(22)
OTHER INFORMATION: Gap in alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,491
FILING DATE: 29-MAY-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.0
Matches 8; Conservative
    96 ASILAVRVLD 105
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                                                              RESULT 13
5472855-6
;Patent No. 5472855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 279
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US-09-698-286A-10
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Sequence 369042, Application US/10425115
Publication No. US20040214272A1
EMBERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Los Novalic, David K.
APPLICANT: Cao, Youngwei
TITLE OF INVENTION: Palants
TITLE OF INVENTION: Palants
TITLE OF INVENTION: Palants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
ISBOGTH: 183
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Pred. No. 7.9;
0; Mismatches 1; Indels
6 US-10-437-963-201347

6 US-10-737-963-175236

6 US-10-369-493-17091

4 US-10-369-493-17091

4 US-10-403-105-9

6 US-10-403-105-9

6 US-10-403-105-9

6 US-10-369-493-7093

5 US-10-369-493-7093

5 US-10-369-493-7093

6 US-10-425-114-70274

6 US-10-369-493-7093

7 US-10-369-493-7093

7 US-10-2124-9728-5583

8 US-10-2124-6285

9 US-10-282-1224-64830

10 US-10-282-1224-6493

10 US-10-282-1224-6493

10 US-10-282-1224-6491

10 US-10-282-1224-6491

10 US-10-282-1224-63141

10 US-10-282-1224-63141
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US-10-425-115-369042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(183)
OTHER INFORMATION: unsure at all Xaa locations
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90.0%;
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Best Local Similarity 90.0
Matches 9, Conservative
                                                                                                   341
6421
6671
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2044
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3331
3358
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3367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-10-425-115-369042
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Sequence 45544, App
Sequence 45544, A
Sequence 208239,
Sequence 120758,
Sequence 14688,
Sequence 15165, A
Sequence 11406, A
Sequence 11635, A
Sequence 11635, A
Sequence 11635, A
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                                                                                                                 October 14, 2005, 16:20:10; Search time 78:2031 Seconds (without alignments) 58.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/NCT NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-389-566-831
US-10-425-114-45544
US-10-425-115-208229
US-10-425-115-208239
US-10-437-963-120758
US-10-369-493-14688
US-10-369-493-14406
US-10-369-493-14406
US-10-369-493-1406
US-10-369-493-11635
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Maximum Match 100%
Listing first 45 summaries
                                                                                  protein search, using sw model
                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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Sequence 63141, Sequence 53, App Sequence 53, App

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Gaps

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74.0%;
72.7%;
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72.7%;
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Best Local Similarity 72.7.
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Best Local Similarity 72.7
Matches 8; Conservative
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ORGANISM: Zea mays
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JS-10-425-115-208229
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 45544
                      Sequence 831, Application US/10389566

Publication No. US2004002202A1

GENERAL INFORMATION:

APPLICANT: Monsanto Technology, LLC

APPLICANT: Monsanto Technology, LLC

TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants

FILE REPERENCE: 38-77(5290)D

CURRENT APPLICATION NUMBER: US 60/385,301

PRIOR APPLICATION NUMBER: US 60/385,301

PRIOR FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: US 60/391,786

PRIOR APPLICATION NUMBER: US 60/391,786

PRIOR APPLICATION NUMBER: US 60/392,018

PRIOR APPLICATION NUMBER: US 60/392,018

PRIOR APPLICATION NUMBER: 2002-06-26

NUMBER OF SEQ ID NOS: 2459

SEQ ID NOS: 2459

SEQ ID NO 831

LENGTH: 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (103)...(104)
CTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 15; Length 408;
Pred. No. 73;
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US-10-425-114-45544
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; Sequence 45544, Application US/10425114
; Publication No. US20040034888A1
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Zea mays
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58 ANIADTRVLDY 68

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Sequence 208239, Application US/10425115

Sequence 208239, Application US/10425115

Sequence 208239, Application US/10425115

Bublication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei
TITLE OF INVENTION: No.Leic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: No.Leic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: No.Leic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: No.Leic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: No.Leic Acid Molecules and Other Molecules Associated With
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 208239

LENGTH: 694
                                                                       APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Avou, Yihua
APPLICANT: Avou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 369326
LENGTH: 573
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Pred. No. 1.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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US-10-425-115-208229
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US-10-425-115-208239
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Pred. No. 1e+02;
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; Sequence 120758, Application US/10437963
; Publication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Rovalic, David K.
; APPLICANT: Zhou, Yihua
Sequence 208229, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Gho, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT PILING NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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72.0%; Score 36; DB 15; Length 652;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels
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Pred. No. 1.9e+02;
2; Mismatches 2;
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15165
LENGTH: 652
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Publication No. US20030233675A1
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US-10-369-493-14406
                                                                                                                                                                                       ) ORGANISM: Agrobacterium tumefaciens US-10-369-493-15165
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Best Local Similarity 63...
7; Conservative
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255 AATAARRIDY 265
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US-10-369-493-11635
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sequence 1468 Application US/10369493

publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14688

LENGTH: 652
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei, Wu, Wei
APPLICANT: Bucharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2016321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 120758
LENGTH: 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
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Pred. No. 2.3e+02;
2; Mismatches 1; Indels
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Pred. No. 1.9e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2384C.1.pep
US-10-437-963-120758
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Sequence 15165, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14688
                                                                                                                                                                                                                                                                                                                                                                                                   74.0%;
70.0%;
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63.6%;
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Best Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 70.0
Matches 7, Conservative
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                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Oryza sativa
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APPLICANT: Li, Ping to Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221) 8 CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 175236 LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38892, Application US/10767701
| Sequence 38892, Application US/10767701
| Publication No. US20040172684A1
| GENERAL INFORMATION:
| APPLICANT: Kovalic, David K. APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
| FILE REFERENCE: 38-21(55535) B | CURRENT APPLICATION NUMBER: US/10/767,701 |
| CURRENT APPLICATION NUMBER: US/10/767,701 |
| CURRENT PILING DATE: 2004-01-29 |
| SEQ ID NOS: 63128 |
| SEQ ID NOS: 63128 |
| LENGTH: 198
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                                                                            Length 45;
                                                                                                              1; Indels
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ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C77436_1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_73100C.1.pep
US-10-437-963-175236
      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_96731C.1.pep
US-10-437-963-201347
                                                                        Score 35; DB 16;
Pred. No. 18;
0; Mismatches 1
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OTHER INFORMATION: unsure at all Xaa locations
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Sequence 175236, Application US/10437963
; Sediation No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                            70.0%;
                                                                                                                  Conservative
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34 ASLAAARVSD 43
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ORGANISM: Oryza sativa
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Best Local Similarity
Matches 8; Conserv
                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
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    FEATURE:
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Sequence 201347, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Vinua

APPLICANT: Cao, Vongwei

APPLICANT: Bunkharov, Andrey A.

APPLICANT: Bunkharov, Andrey A.

APPLICANT: Bunkharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 39-21(53221)B

CURRENT FILING DATE: 2003-05-14

CURRENT FILING DATE: 2003-05-14

MUNDER OF SEQ ID NOS: 204966

SEQ ID NO 201347

LENGTH: 45
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                                                                                          72.0%; Score 36; DB 15; Length 656; 63.6%; Pred. No. 1.9e+02; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.0%; Score 36; DB 16; Length 10
80.0%; Pred. No. 3.2e+02;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Clone ID: PAT_MRT4530_85594C.1.pep
US-10-437-963-189048
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11635
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Best Local Similarity 80.0-
                                                                          Query Match
Best Local Similarity 63.00
Particle 7; Conservative
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255 AATAAARAIDY 265
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116 ASLAALRVLD 125
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ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
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JULIO 1991, Application US/10369493

J. Sequence 17091, Application US/10369493

J. Sequence 17091, Application US/10369493

J. Publication No. US20030233675A1

J. Publication No. US20030233675A1

J. Publication No. US20030233675A1

J. Publication No. US2003023675A1

J. APPLICANT: Gareary Steven C.

J. APPLICANT: Gldman, Barry S.

J. PUBLICANT: Gldman, Barry S.

J. TILE DF INVENTION: PLANTS WITH IMPROVED PROPERTIES

J. PRIOR APPLICATION NUMBER: US 60/360,039

J. PRIOR FILING DATE: 2003-02-28

J. RIOR APPLICATION NUMBER: US 60/360,039

J. RIOR PILING DATE: 2003-02-24

J. NUMBER OF SEQ ID NOS: 47374

J. SEQ ID NO 17091

J. TYPE: PRT

J. TYPE
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                                                                                                          Query Match 68.0%; Score 34; DB 16; Length 198; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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114 AARVLDY 120
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US-10-767-701-38892
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US-10-369-493-17091
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Search completed: October 14, 2005, 17:00:43 Job time : 79.2031 secs

1 ASIAAARVLD 10 |:||||| || 100 ATIAAARKLD 109

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October 14, 2005, 15:51:19 ; Search time 99.9375 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

SGSTSNIGNNYVS 13 US-10-614-959-13 66 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

BB DB Minimum I Maximum I

length: 0 length: 2000000000 sed

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:*geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	uo	Anti-fact	Anti-adip	Human BLy	Single ch	Neurokini	Neurokini	Human BLy	Human CMO	Single ch	Neurokini	Neurokini	Neurokini	Human BLy	Single ch	TNF proli	Chemokine	Neurokini	Neurokini	Human BLy						
	Description	Aay79071	Aau02544	Aau02558	Aau02612	Aau02627	Aau02629	Aau02542	Aau02551	Abp45887	Adg96714	Adg34301	Adg34317	Abp45916	Aao31147	Adg96743	Adg34310	Adg34306	Adg34303	Abp45915	Adg96742	Adg98057	Ade83862	Adg34308	Adg34313	Abp45902
Q.																										
SUMMAKIES	ΩI	AAY79071	AAU02544	AAU02558	AAU02612	AAU02627	AAU02629	AAU02542	AAU02551	ABP45887	ADG96714	ADG34301	ADG34317	ABP45916	AA031147	ADG96743	ADG34310	ADG34306	ADG34303	ABP45915	ADG96742	ADG98057	ADE83862	ADG34308	ADG34313	ABP45902
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	Match Length	13	109	110	110	110	110	111	111	240	240	242	242	243	243	243	243	243	244	245	245	245	245	245	245	246
, 2 2	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Abp45906 Human BLy Adg96733 Single ch Adg96729 Single ch		Human Human Human Kuman		Adg96259 Single ch Adg96750 Single ch Adg96523 Single ch Ade83874 Chemokine Adg34304 Neurokini
ABP45906 ADG96733 ADG96729	ADE83872 ABP45671 ABP45432 ABP45923	ABP45917 ABP45696 ABP45888 ADG30413	ADG30455 ADG96715 ADG96498 ADG96744	ADG96259 ADG96750 ADG96523 ADE83874 ADG34304
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25 27 28 28	38 H 8 8	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	37 38 40	4 4 4 4 4 1 5 6 4 7

# ALIGNMENTS

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Complementarity determining region 1; CDR1; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastesis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.
                                                             Anti-factor IX/IXa antibody L chain V domain CDR1 amino acid sequence.
AAY79071 standard; peptide; 13 AA.
                                         12-JUN-2000 (first entry)
                     AAY79071;
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WO200012562-A1. Homo sapiens. 09-MAR-2000.

99WO-US019453. 98US-0098233P. 99US-0122767P. 26-AUG-1999; 28-AUG-1998; 03-MAR-1999;

(GETH ) GENENTECH INC.

Hass PE, Judice JK, Kirchhofer D; Devaux B, Eaton DL, Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 1 (CDR1) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. To Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angiopatery (PrCA), stroke, tumour growth, invasion or metastesis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fat;
                                                                                                                                                                                                                                                Length 13;
                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody, adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-adipocyte monoclonal antibody light chain, FAT 31.
                                                                                                                                                                                                                                                Score 66; DB 3; I
Pred. No. 0.00029;
                                                                                                                                                                                                                             (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU02544 standard; protein; 109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaughan TJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2000; 2000WO-GB003900.
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                                                                                                                                                                                                                                                                                                                                                       1 SGSTSNIGNNYVS 13
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Best Local Similarity 100.
Matches 13; Conservative
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N-PSDB; AAS03444.
                                                                                                                                                                                                           Sequence 13 AA;
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
of complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
cused in methods of diagnosis in human subjects e.g. to determine the
cused in methods can rievel of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
corrected the present disposite can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                                                        Gaps
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for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                  Score 66; DB 4; Length 109;
Pred. No. 0.0026;
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                      Anti-adipocyte monoclonal antibody light chain, FAT 44.
                                                                                                    ; Pred. No. 0.0026; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                               AAU02558 standard; protein; 110 AA.
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                                                                                   100.0%;
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                                                                                                                        13; Conservative
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Best Local Similarity
                                                                                                      Local Similarity
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                                                    Sequence 109 AA;
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                                                                                       Query Match
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AAU02558
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Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.

Anti-adipocyte monoclonal antibody light chain, FAT 112.

(first entry)

29-AUG-2001

AAU02627 standard; protein; 110 AA.

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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, invention. The antibodyte was an interest on the antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody or an be used as therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
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100.0%; Pred. No. 0.0026;
iive 0; Mismatches 0
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                                                                                                                                                                                                                               AAU02612 standard; protein; 110 AA.
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13
                                      23 SGSTSNIGNNYVS 35
SGSTSNIGNNYVS
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Best Local 9
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ID AA
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Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related

Claim 1; Page 172; 182pp; English.

diseases

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

99US-0158812P

12-OCT-1999;

11-OCT-2000; 2000WO-GB003900

NO200127279-A1

19-APR-2001

Homo sapiens.

Vaughan TJ;

Main SH,

Edwards BM,

WPI; 2001-282031/29. N-PSDB; AAS03527.

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ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the far mass of an obesse patient or the antibody
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by complement mediated lysis. The antibodies may be labeled with a
cetcable label such as radiolabel, fluorescent or chemical group and
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creamine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
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con different types of fat deposite can also be produced e.g. intra-
abdominal fat associated with heart disease
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Pred. No. 0.0026;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Best Local Simi]
Matches 13; (
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0; Indels

SGSTSNIGNNYVS 35 1 SGSTSNIGNNYVS 13 13; Conservative

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RESULT 5 AAU02627

Matches

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cequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used as an extract the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                               Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                        AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
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                                                                                                                   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 118-119; 182pp; English.
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                                                                                                                                                                 Vaughan TJ;
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                            11-OCT-2000; 2000WO-GB003900.
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Best Local Similarity
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N-PSDB; AAS03442
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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
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chugs directly to the fat mass of an obese patient or the antibody
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adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
con different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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100.0%; Pred. No. 0.0026;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                          (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02542 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                       Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 173; 182pp; English.
                                                                                                                                                                                                            11-OCT-2000; 2000WO-GB003900.
                                                                                                                                                                                                                                                            99US-0158812P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
                                                                                                                                                                                                                                                                                                                                                       Edwards BM, Main SH,
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-282031/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 110 AA;
                                                                                                                   WO200127279-A1
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                                                                                                                                                                                                                                                            12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2001
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                                                                                                                                                                 19-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases.
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Matches

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Gaps

Hilbert

Vaughan T,

Choi GH,

Barash SC,

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Ruben SM,
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                                                                                                                     ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a chectable label such as radiolabel; fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies can also be produced e.g. intra-
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; fimunosuppressive; immunostimulat; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   common variable immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 66; DB 4; Length 111;
100.0%; Pred. No. 0.0027;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                             abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human BLyS binding scFv SEQ ID 1898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP45887 standard; protein; 240 AA
                                                                                                Claim 1; Page 124; 182pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0212210P.
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2001US-0276248P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L5-JUN-2001; 2001WO-US019110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              24 SGSTSNIGNNYVS 36
                                                                                                                                                                                                                                                                                                                                                                                                                               1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
             2001-282031/29
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
tes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                       Sequence 111 AA;
                       N-PSDB; AAS0345
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16-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP45887;
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                         diseases
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity on be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant appression of Alexandra and activity such as cancer, immune, and autoimmune disorders and diseases. e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (cVID) and acquired immunodeficiency syndrome (AlDS)). ABB43990-ABB47228 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g.
                                                         Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain antibody that immunospecifically binds BLyS SeqID 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody, B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; antiasthmatic; antiallergic; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66; DB 5;
Pred. No. 0.0059;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaughan TJ,
                                                                                                                                                            Claim 1; Page 2666-2667; 3148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG96714 standard; protein; 240 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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19-DEC-2001; 2001US-0340817P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-2002; 2002WO-US036496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-505530/47.
WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention
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26-FEB-2004
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                                                                   invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154
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                                                                                                                      Query Match
                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                                                           ઠે
                                             This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to C chromosome 1344 and encodes a protein that is a member of the tumour chromosome 1344 and encodes both in vivo and in vitro B cell necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable compared invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphome Accordingly, they can be described as exhibiting various cutivities such as antirheumatic, antiallergic and cytostatic. This collypholises us antirheumatic, antiallergic and cytostatic. This collypholise sequence data is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format contractly from WIPO at ftp.wipo.int/published pot_equences.
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; neurokinin B; hypotensive; gynaecological; gene therapy; hypertension; pre-eclampsia; NKB.
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 66; DB 7; Length 240; 100.0%; Pred. No. 0.0059; ive 0; Mismatches 0; Indels
rheumatoid arthritis, asthma and leukemia.
                          Example 1; SEQ ID NO 1898; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID NO 24; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurokinin B antibody SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG34301 standard; protein; 242 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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ADG34301
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The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypotension or precelampsia. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological estivity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or preclampsia. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody; neurokinin B; hypotensive; gynaecological; gene therapy; hypertension; pre-eclampsia; NKB.
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                                                                                                                                                                                                                                                                                     100.0%; Score 66; DB 8; Length 242; ilarity 100.0%; Pred. No. 0.006; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG34317 standard; protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurokinin B antibody SEQ ID NO:40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 100.
Matches 13; Conservative
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N-PSDB; ADG34298.
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ses 13; Conserv
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                                                                                                                                                                                                                                     Sequence 242 AA;
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Human, protein coordinate data, heavy chain variable domain, VH; cancer, complementarity determining region; CDR; light chain variable domain; VL; TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5; DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand, Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma; gidloblastoma; graft versus host disease; antibody therapy; nootropic; AIDS; acquired immune deficiency syndrome; neurodegenerative disorder; immunosuppressive; neuroprotective; antibody therapy; antibody.

Human CM085C11 scFv protein that specifically binds TR7.

06-OCT-2003 (first entry)

AAO31147;

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BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiALDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; ALDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP4399-ABF47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes novel antibodies that immunospecifically bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choi GH, Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 2700-2701; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                  Human BLyS binding scFv SEQ ID 1927.
ABP45916 standard; protein; 243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2001; 2001WO-US019110
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                                                                          (first entry)
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                            19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                      10-JAN-2002
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                                      ABP45916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated antibody or its fragments such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 66; DB 6; Length 243; 100.0%; Pred. No. 0.006; ive 0; Mismatches 0; Indels
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nes 13; Conservative
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binds TR7
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lung or

ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lu gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host New antibody or its fragment, useful for treating, preventing or

Claim 2; Page 288; 301pp; English.

disease, AIDS.

Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;

WPI; 2003-569250/53. N-PSDB; AAL62844.

2001US-0341237P. 2002US-0369877P. 2002US-0384828P. 2002US-0396591P.

04-JUN-2002; 20-DEC-2001; 05-APR-2002;

19-DEC-2002; 2002WO-US040597

WO2003054216-A2.

03-JUL-2003

Homo sapiens

15-AUG-2002; 2002US-0403370P.

(HUMA-) HUMAN GENOME SCI INC

RESULT 15

AAO31147 standard; protein; 243 AA.

SGSTSNIGNNYVS 167

155

RESULT 14 AAO31147 ID AAO3

1 SGSTSNIGNNYVS 13

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ö Gaps ö 100.0%; Score 66; DB 5; Length 243; 100.0%; Pred. No. 0.006; ive 0; Mismatches 0; Indels

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Job time : 100.938 secs

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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13d34 and encodes a protein that is a member of the tumour corrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFv8) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods of for the detection, diagnosis and prognosis of diseases related to the about, these compositions are useful for identifying immune disorders cut, including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis infectious diseases such as ALDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various antibularmatory antiather such as antitheumatic, antiathritic, neuroprotective, misc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory, antiasthmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                                                                   Single chain antibody that immunospecifically binds BLyS SeqID 1927
                                                                                                                                                                                                                                                                                                                                      antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 66; DB 7; Length 243; 100.0%; Pred. No. 0.006; ive 0; Mismatches 0; Indels
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                                       ADG96743 standard; protein; 243 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
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                                                                                                                                                                                            (first entry)
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                            11-MAR-2004
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                                                                                                                      ADG96743;
ADG96743

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Search completed: October 14, 2005, 16:12:41

155 SGSTSNIGNNYVS 167

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Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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protein search, using sw model OM protein - October 14, 2005, 16:02:59 ; Search time 18.0781 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

1 SGSTSNIGNNYVS 13 US-10-614-959-13 66 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	OI s			: S19664			-	-		-		LIHUNW											: S36258			82	: A44151	B4	S25754	SI
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	Length	86	111		113			130	130	111	131	111	98	111	129	130	109	98	234	112	216	98	110	112	117	233	112	112	235	235
de	Query	93		93	93.9	93	93		86	84	84	83	80	80	80	80	78	75	74		69	68	68	68.2	68.2	œ	66.7	9	66.7	
	Score	62	62	62	62	62	62	59	57	26	56	52	53	53	53	53	52	20	49	48	46	45	45	45	45	45	44	44	44	43.5
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Ig lambda chain pr Ig lambda chain V gag, pol and env p	hypochetical prote Ig light chain V-J Ig lambda chain V- Ig lambda chain -	uncharacterized co Ig lambda chain - Ig lambda chain V	ig lambda chain v- Ig lambda chain V- 5-aminolevulinate Ig lambda chain V-	Ig lambda chain V- Ig lambda chain NI
S49571 S23626 T18572	G71609 S57428 S57408 S25744	F96997 S36054 B46516	LSHULI LIHUMM A71646 LIHUWA	L1HUHA JE0246
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95 149 2272	2500 110 110 233	348 107	112	112
65.52	63.6 63.6 63.6	63.6 62.1	62.1 62.1 60.6	60.6 60.6
444	4 4 4 4 W W W W	444	4 4 4 4 4 4 1 0	4 4 0 0
330	33 33 65	338	4 4 4 4 0 1 2 6	44 45

## ALIGNMENTS

336050
Ig lambda chain - human (fragment)
CjSpecies: Homo sapiens (man)
CjSpecies: Homo sapiens (man)
CjBecies: S2-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
CjAccession: S36050
RjWilliams, S.C.
BiWilliams, S.C.
AjAccession: S36050
AjReference number: S36046
AjReference number: S36050
AjReference number: DNA
AjResidues: 1-98 <WILD

A,Cross-references: EMBL:Z22191, NID:g312298, PIDN:CAA80201.1; PID:g312299 C,Superfamily: immunoglobulin V region; immunoglobulin homology C,Ekeywords: heterotetramer; immunoglobulin P:15-91/Domain: immunoglobulin homology <a href="https://www.referencestramer.htm.noglobulin">https://www.referencestramer.htm.noglobulin</a> P:15-91/Domain: immunoglobulin homology <a href="https://www.referencestramer.htm.noglobulin">https://www.referencestramer.htm.noglobulin</a> homology <a href="https://www.referencestramer.htm.noglobulin</a> homology <a href="https://www.referencestramer.htm.noglobulin</a> homo

Gaps ö Length 98; 0; Indels Score 62; DB 2; Pred. No. 0.001; 1; Mismatches 93.9%; Query Match Best Local Similarity 92.3 Matches 12; Conservative

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1 SGSTSNIGNNYVS 13 23 SGSSSNIGNNYVS 35 셤 ઠે

RESULT 2

847009

19 lambda chain V1-J3 region - human C;Species: Homo sapiens (man) S; Factes: Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000 R;Mahmoudi, M.; Gasyna, B.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E. submitted to the EMBL Data Library, July 1994 A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin A;Reference number: 847009 A;Reference number: 847009 A;Residues: 1-111 < MAH>
A;Residues: 1-111 < MAH>
A;Molecule type: mRNA A;Residues: 1-111 < MAH>
A;Residues: 1-111 < MAH>
A;Residues: 1-111 < MAH>
A;Residues: Iimmunoglobulin V region; immunoglobulin homology C;Supwords: heteroctetramer; immunoglobulin homology < IMM>
F;15-91/Domain: immunoglobulin homology < IMM>

Gaps ö Length 111; Query Match 93.9%; Score 62; DB 2; Length 111 Best Local Similarity 92.3%; Pred. No. 0.0011; Matches 12; Conservative 1; Mismatches 0; Indels

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1 SGSTSNIGNNYVS 13

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Gaps

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A;Molecule type: mRNA
A;Residues: 1-225 <KKIS.)
A;Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395
A;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
A;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A;Reference number: S04601; MUID:89296497; PMID:2500644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S09712 "Lovacoure_revision in-mov-1395 #text_cnange 21-Jan-2000
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Notleotide sequences and three-dimensional modelling of the VH and VL domains A;Reference number: S09710; MUID:90262535; PMID:2111699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Accession: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000 C, Accession: S05270; S04601
R;Kishimoto, T. submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05270
A;Moleculary S05270
A;Moleculary S05270
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C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
                                                                                             A;Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710 CS.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramely F;147-215/Pomain: immunoglobulin homology xIMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X52109; NID:g31454; PIDN:CAA36343.1; PID:g31455 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;34-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-130 < KIS2>
A; Cresidues: 1-130 < KIS2>
A; Cresidues: 1-130 < KIS2>
C; Stoperfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 1-20; Domain: signal sequence #statuus predicted <SIG>
F; 1-23; Product: Ig lambda chain #statuus predicted <MAT>
F; 150-218 / Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                         Length 232;
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. 0.0025;
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Pred. No. 0.0025;
                                                                                                                                                                                                                                                                       1; Mismatches
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               A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-212 <COM>
                                                                                                                                                                                                                      Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.9%;
92.3%;
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92.3%;
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                                                                                                                                                                                                                                                                                                                        1 SGSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                       12; Conservative
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserv
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A;Molecule type: mRNA
A;Residues: 1-130 <HUG>
A;Accession: S25742
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                                                                                                            A29700

Ig lambda chain V region (Zim) - human (fragment)

C,Species: Homo sapiens (man)

C,Species: Homo sapiens (man)

C,Species: Homo sapiens (man)

C,Species: Homo sapiens (man)

C,Species: J1-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000

C,Accession: A29700

R,Eulitz, M.; Breuer, M.; Linke, R.P.

Biol. Chem. Hoppe-Seyler 368, 863-870, 1987

Biol. Chem. Hoppe-Seyler 368, 863-870, 1987

A;Title: Is the formation of AL-type amyloid promoted by structural peculiarities of imm A;Reference number: A29700

A;Molecule type: protein

A;Accession: A29700

A;Molecule type: protein

A;Residues: 1-113 **RUL*

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Reywords: heterotetramer; immunoglobulin

F;14-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.0011;
1; Mismatches 0; Indels
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Pred. No. 0.0012;
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Local Similarity 92.3%;
hes 12; Conservative
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SGSSSNIGNNYVS 35
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Matches 12
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C;Accession: S24321
R;Aucouturier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne, Biochem. J. 285, 149-152, 1992
A;Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr A;Reference number: S24319; MUID:92344562; PMID:1379039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiLanger, B.; Steinmetz-Kayne, M.; Hilschmann, N.
hoppe-Seyler's Z. Physiol. Chem. 349, 345-951, 1968
A.Title: The complete amino acid sequence of Bence-Jones protein New (lambda type). Subg
A.Reference number: A01964; MUID:69060892; PMID:4177823
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A; Cross-references: GDB:119342; OMIM:147240
A; Map position: 22q11.2-22q11.2
C; Complex: An immunoglobulin heteroteramer subunit consists of two identical light (kap hain disulfide bonds: In socset, esten as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < IMM>
F; 15-91/Domain: immunoglobulin homology < IMM>
F; 16-91/Domain: immunoglobulin homology < IMM>
F; 16-91/Domain: immunoglobulin homology < IMM>
F; 16-91/Domain: immunoglobulin predicted
                                                                                                           Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: Si6048; Si6048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig lambda chain V-I region (New) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
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84.6%; Pred. No. 0.015;
tive 1; Mismatches
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C; Comment: This is a Bence Jones protein.
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Matches 11; Conservative
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tes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-131 <AUC>
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S36048
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847185
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: 847185
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: $47181
A;Accession: $47185
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-111 <MCI>
A;Cross-references: EMBL:X79782; NID:9506428; PIDN:CAAS6178.1; PID:9506429
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-90/Domain: immunoglobulin homology <IMM>
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A; Map position: 22q1.2-22q1.2
A; Map position: 22q1.2-22q1.2
Complex: An immunoglobulin herectamer subunit consists of two identical light (kap close) and individual conditions. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-115/Region: sequence #status predicted <SIG>
F; 20-115/Region: V segment
F; 34-110/Domain: immunoglobulin homology <IMM>
F; 116-130/Region: J segment
F; 41-108/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P06316; GB:X01147; NID:g33335; PIDN:CAA25598.1; PID:g758087 C;Genetics:
                                                                                                                                                                                                                                           RESULT 8
LiHUBL
Glambda chain precursor V-I region (BL2) - human
Cj Species: Homo sapiens (man)
CjSpecies: Homo sapiens (man)
CjDate: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
CjAccession: A01966
RjTsujimoto, Y.; Croce, C.M.
Nucleic Acids Res. 12, 8407-8414, 1984
A;Title: Molecular cloning of a human immunoglobulin lambda chain variable sequence.
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89.4%; Score 59; DB 2; Length 130;
84.6%; Pred. No. 0.0045;
ive 2; Mismatches 0; Indels
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Pred. No. 0.013;
1; Mismatches
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Pred. No. 0.01;
2; Mismatches
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84.6%;
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84.6%;
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-130 <TSU>
                               Similarity
        / Mu.
Local S.
11;
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Query Match
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Search completed: October 14, 2005, 16:23:38 Job time : 18.0781 secs
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Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-129 < HAR>
A; Residues: 1-129 < HAR>
A; Cross-references: EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g930121
B; Harindranath, N.; Goldfarb, I.S.; Ikemateu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A; Reference number: S23716; MUID:92031262; PMID:1718404
                      A.Reference number: S36046
A.Accession: S36048
A.Accession: S36048
A.Accession: S36048
A.Accession: S36048
A.Accession: S36048
A.Residues: 1-98 <WIL>
A.Residues: 1-98 <WIL>
A.Residues: 1-98 <WIL>
C.Superferences: EMBL: Z22189; NID: g312294; PIDN: CAA80199.1; PID: g312295; EMBL: Z22190
C.Superferanly: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>
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Ig lambda chain precursor V-J region (clone mAB 67VL) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78058; S23723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 2; Length 98;
Pred. No. 0.037;
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submitted to the EMBL Data Library, April 1993
                                                                                                                                                                                                                                                                                                                                                                                             80.3%;
83.3%;
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R; Harindranath, N.
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LIHUNG
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A;Molecule type: mRNA
A;Residues: 1-130 <HAR>
A;Cross-references: EMBL:X54438; NID:g37920; PIDN:CAA38307.1; PID:g37921
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
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C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78057; S23722
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A;Residues: 19-129 cHAM>
A;Residues: 19-129 cHAM>
A;Cross-references: EMBL:X54446
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: immunoglobulin
F;1-18/Domain: signal sequence (fragment) #status predicted <SIG>
F;19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F;33-109/Domain: immunoglobulin homology <IMM>
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F;20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>
F;34-110/Domain: immunoglobulin homology <IMM>
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A;Residues: 20-130 <HAM-
A;Croser_references: EMBL:X54438
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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A, Reference number: $23716; MUID: 92031262; PMID: 1718404
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Pred. No. 0.049;
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Pred. No. 0.049;
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A;Reference number: S78051
A;Accession: S78057
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83.3%;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 14, 2005, 15:51:44; Search time 86.5312 Seconds (without alignments) 76.932 Million cell updates/sec Run on:

US-10-614-959-13 66 1 SGSTSNIGNNYVS 13 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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			UMAN			UMAN		UMAN	UMAN										CAEEL					ELEEL	UMAN	UMAN		RICPR					
	Ü		LV1G HUMAN	QBIZDB	Q8TE63	LV1C HUMAN	096SB0	LV1D HUMAN	LV1 I HUMAN	66NI90	QBNEJ1	Q6DHW4	OGGMW6	Q87LH3	Q7SCJ5	Q8JRX2	O7WZN9	Q9W4M4	YL52 C	017329	096223	Q6GMV7	Q97KX3	ACES E	LV6D HUMAN	LV1H HUMAN	Q9VRW7	HEM1 R	Q68V <u>S</u> 3	Q6BK59	Q7RRT8	Q95SG4	Q9W117
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æ	Query Match		86.4	84.8	83.3	83.3	80.3	80.3	78.8	78.8	77.3	74.2	68.2	66.7	66.7	66.7	65.2	65.2	65.2	65.2	65.2	63.6	63.6	63.6	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1
	Score		57	26	55	55	53	53	52	52	51	49	45	44	44	44	43	43	43	43	43	42	42	42	41	41	41	41	41	41	41	41	41
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# ALIGNMENTS

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HUMAN STANDARD; PRI P06316, 01-JAN-1988 (Rel. 06, Created) 11-JAN-1998 (Rel. 06, Last sequen 115-JUL-1999 (Rel. 38, Last annotes 121-JAN-1998 (Rel. 38, Last annotes 121-JAN-1999 (Rel. 38, Let annotes 121-JAN-1999 (Rel. 38, Let annotes 121-JAN-1999 (Rel. 38, Let annotes 121-JAN-1999 (Rel. 39, Let annotes 121-JAN-199 (Rel. 39, Let annotes	n Similarity 84. 11, Conservative
HUMAN   16,     16,     16,     16,     17,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     19,     10,     10,     10,     10,     10,     10,     10,     10,     10,     10,     10,     10,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,     11,	th Simi 11,
HUMAN  FUGGIG;  O1-JAN-1988 (Rel  O1-JAN-1988 (Rel  O1-JAN-1988 (Rel  IS-JUL-1999 (Rel  IS-JUL-1999 (Rel  IS Jambda chain  Homo sapiens (Huu  MEDLINES (RES  RELIARYOLE FROM N.)  REDILINES (RES  SEQUENCE FROM N.)  REDILINES (RES  REDILINES (RES  TRUJINDES  TRUJINDES (RES  TRUJINDES  TRUJINDE	gat
RESULT 1  LV1G HUMAN  ALC FORST  DDT 01-JAM  DDT 01-JAM  DDT 01-JAM  DDT 01-JAM  DDT 01-JAM  DDT 01-JAM  COC Mamma  COC Mamma  COC TISS	Query M Best Lo Matches
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1 SGSTSNIGNNYVS 13
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                                                                                                                                                                                                    LV1C HUMAN
P01701;
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SEQUENCE
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Q96SB0;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11mmunglobulin light chain variable region (Fragment).
12mmos appiens (Human).
13mmos Appiens (Human).
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-thyroglobulin light chain variable region (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.8%; Score 56; DB 2; Length 101; 84.6%; Pred. No. 0.079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jang Y.-J., Chung J., Park J.-Y.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 AA; 10374 MW; 1506C2D9AACBA793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 AA; 11479 MW; 599D1628F8F5437C CRC64;
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                                                                                                                                             101 AA
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                                                                                                                                             PRT;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                             PRELIMINARY;
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42 SGSSSNIGNDYVS
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE
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Q81ZD8;
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MEDLINE=69060892; PubMed=4177823;
MEDLINE=69060892; PubMed=4177823;
Langer B., Steinmetz-Kayne M., Hilschmann N.;
Langer B., Steinmetz-Kayne M., Hilschmann N.;
The complete amino acid sequence of Bence Jones protein New (lambda-type). The lambda-type.";
Type). Subgroups in the variable part of immunoglobulin L-chains of the lambda-type.";
HOPPE-Seyler's Z. Physiol. Chem. 349:945-951(1968).

MISCELLANEOUS: This is a Bence-Jones protein.
PIR, A01964; LIHUWW.
R HSSP, P01703; 7FAB.
GO, GO:0005576; C:extracellular; NAS.
GO, GO:0005955; P:immune response; NAS.
RO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR00710; Ig-like.
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin lambda light chain variable region (Fragment).
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MEDLINE-98375893; PubMed-9712075;
Adderson B.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polytractive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
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SMART, SM00406; ig; 1.

SMART, SM00406; iGv; 1.

PROSITE; PSS0835; IG_LIKE; 1.

Bence-Jones protein; Direct protein sequencing;

Immunoglobulin V region; Pyrrolidone carboxylic acid.

NOWAIN

1 105

Provinidone carboxylic a
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Pred. No. 0.13;
                                                                                                                                                                                                                                       21-JUJ-1986 (Rel. 01, Created)
21-JUJ-1986 (Rel. 01, Last sequence update)
05-JUJ-2004 (Rel. 44, Last annotation update)
Ig lambda chain V-I region NEW.
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76.9%;
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SGTSSNIGNNFVS 35
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tes 10; Conservative
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the sequenced

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TISSUB-PADGECES;

MEDINE-21388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rlauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

La ctapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                           Toft K.G., Sletten K., Husby G.; "The amino-acid sequence of the variable region of a carbohydrate-containing amyloid fibril protein BPS (Immunoglobulin light chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.8%; Score 52; DB 1; Length 109; 83.3%; Pred. No. 0.42;
                                                                                                                                                                                                                    Pici. Chem. Hoppe-Seyler 366:617-625(1985).
-I- MISCELLANEOUS: Residues 1-2, 56-62, and 74-78 and peptides were positioned by homology.
-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP: P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 109
109 AA; 11414 MW; 556A313E24D5AC73 CRC64;
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N-linked (GlcNAc. ..).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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SMART; SM00406; IGV; 1.
SMO31TE; PS50815; IG_LIKE; 1.
Amyloid; Direct protein sequencing; Glycoprotein; Immnoglobulin V region.
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
103-JUL-2004 (Rel. 17 region EPS.
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003596; IG-V.
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                            MEDLINE=86000126; PubMed=3929803;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 SGSSSNIGKNYV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
Les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGLC2 protein.
Name=IGLC2;
                                                                                                                                                                                                          type lambda).
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SEQUENCE
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                                                                                                                              SEQUENCE
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Q61N99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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                                                                                                                                                                                                              Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83186114; PubMed-6404900;
Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
Shimizu A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.3%; Score 53; DB 1; Length 111; 76.9%; Pred. No. 0.29;
                                                                                                                                                                          80.3%; Score 53; DB 2; Length 108; 83.3%; Pred. No. 0.28; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig-like.
Pyrrolidone carboxylic acid.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 111
111 AA; 11454 MW; A21C6121C18A61E0 CRC64;
                                                                                                                                            108 AA; 11594 MW; F4B5DC478A043F48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfan; PP00047; ig; i. --
MART; SM00406; IG; i. --
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid. -- 116.
                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 AA
                                                                                                                                                                                                                                                                                                                                                             111 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
           J. Immunol. 161:2020-2011(1998).
EMBL; U96394; AAB68783.1; --
PDB; IKU4; Model; L=1-108.
InterPro; IPR007110; Ig-like.
InterPro; IPR00356; Ig-v.
SMART; SM00406; IGv; I.
PROSITE; PS50835; IG_LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVII_HUMAN
ID LVII HUMAN STANDARD;
AC P06888;
DT 01-JAN-1988 (Rel. 06, Created)
 antibody V region genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 SGSSSNIGDNFVS 35
                                                                                                                                                                     Ouery Match
Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                            1 SGSTSNIGNNYV 12
                                                                                                                                                                                                                                                           23 SGSSSNIGSNYV 34
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Best Local Similarity
10; Conserva
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SEQUENCE
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NON TER
SEQÜENCE
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RESULT 7

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LV1D_HUMAN

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Sest Local Similarity
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                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
SEQUENCE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004
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25-OCT-2004
                                                                             TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=223825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE=223825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
M. Strausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
M. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
M. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Parage C.,
M. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Noriski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.8%; Score 52; DB 2; Length 235; 76.9%; Pred. No. 0.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                             Straubberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072392; AAH72392.1; -.
INTERPYO; IPRO03599; Ig.
InterPro; IPRO0310; Ig-like.
InterPro; IPRO03597; Ig_c1.
InterPro; IPRO03596; Ig_WHC.
InterPro; IPRO03596; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00409; IG; 2.
SMART; SM004007; IGc1; 1.
SMART; SM004007; IGc1; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0029035; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 235 AA; Z4888 MW; 90C95D5E87A6BCC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2002 (TrEMBLrel. 22,
01-0CT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 SGRSSNIGNSYVS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.8
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Human)
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Q8NEJ1
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ESUGENCE From A. B. Cells;

XX TISSUB—Primary B-Cells;

XX Strausberg R.L., Faingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Faingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Faingold E.A., Grouse L.H., Derge J.G.,

XI Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heibeh F.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heibeh F.,

XX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Stapleton M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

XX Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

XX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

XX Jones S.J., Marra M.A.,

XX 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 236;
                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030984; AAH30984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC075843; AAH75843.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 protein.
236 AA; 25024 MW; 1703B77942630E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 2;
Pred. No. 1.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 AA.
                                                                                                                                                                                                                                                                                            HSSP; PO1703; 7FAB.

InterPro; IPR007110; Ig-11ke.

InterPro; IPR003199; Ig_c1.

InterPro; IPR003596; Ig_wHC.

InterPro; IPR003596; Ig_wHC.

InterPro; IPR003596; Ig_wHC.

SMART; SW00406; IGw; 1.

PROSITE; PS00290; IG_LKE; 2.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 28, (TrEMBLrel. 28, (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SGSTSNIGNNYV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 SGSRSNIGSNYV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissum=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. Homo sapiens (Human).
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Q87LH3
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Q87LH3
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    SKRR
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XX Exaubberg R.C. Feingold E.A. Grouse L.H., Derge J.G.,

XX Exaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altsubner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

B. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B. Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Andrinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                           74.2%; Score 49; DB 2; Length 237;
83.3%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC073784, AH773784.1;
InterPro; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003596; Ig.w.
Pfam; PF00654; Cl.set; I.
                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 237 AA; 25108 MW; 6814170F7E784825 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 AA
                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                              Pfam; PP00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00220; IG_MHC; UNKXVOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; 1.
                                                                                                                                                                                                                                                                                                   Local Similarity 83.3
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                         1 SGSTSNIGNNYV 12
                                                                                                                                                                                                                                                                                                                                                                                                    42 SGSSSNIGINYV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGGMW6;
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OGGNW6

OGGNW6

DT 05-JU

DT 05-JU

DE HYPOEL

OG BERARY

OC BERAR
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PSEQUENCE FROM N.A.

RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

RX MELINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

RA Makino K., Oshima K., Kurokawa K., Yamashita A., Kubota Y., Kimura S., Raharina Y., Najima M., Nahano M., Yamashita A., Kubota Y., Kimura S., RA Yasunaga T., Honda T., Shinagawa H., Hattori M., iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";

"EmBL; APOS0502: BAC60902.1; -.

BRBL; ADOS0502: BAC60902.1; -.

GO; GO:0016491; P:oxidoreductase activity; IEA.

GO; GO:0016491; P:oxidoreductase activity; IEA.

GO; GO:0016491; P:oxidoreductase activity; IEA.

GO; GO:00106491; P:oxidoreductase activity; IEA.

GO; GO:00106491; P:oxidoreductase activity; IEA.
                                                                                                                                                                                             Gaps
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
NCBL_TaxID=670;
                                                                                                                                       Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 221;
                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 235 AA; 24803 MW; 058805F61118F1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 AA; 23803 MW; D545E953C9AB3A2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Last annotation update)
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66.7%; Pred. No. 20;
:ive 2; Mismatches 2
                                                                                                                                       68.2%; Score 45; DB 2; 69.2%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                               221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 AA.
                                                                                                                                                                                             3; Mismatches
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
butative short-chain dehydrogenase.
OrderedLocusNames-VP2639;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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InterPro; IPR002347; Adh_short_C2.
Pfam; PF00106; adh_short; 1.
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein.
                                                                                                                                                                                                                                                    1 SGSTSNIGNNYVS 13
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Best Local Similarity 66...
8; Conservative
                                                                                                                                       Query Match
Best Local Similarity 69.23
Matches 9; Conservative
                                                                                                                                                                                                                                                                                    SGSSSNIGSNSVN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALANIGNGYVS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrio parahaemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
SEQUENCE 221 AA;
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A Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Bikins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Schulte U., Schlitzennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., A. Kamal M., Kamvysselis M., Maucell E., Bleike C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Merzenberg R.L., Perkins D.D., Kroken S., Coponi C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seller S., Dunlap J., Radford A., Aramayo R., Arden O., Plamann M., Seller S., Dunlap J., Freitag M., Aramayo R., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 0:0-0(2003).

-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AABX01000101; EAA34466.1; -16.

GO, GO:0005576; C:extracellular; IEA.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
Stal_TaxID=192584;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 66.7%; Score 44; DB 2; Length 326; Local Similarity 61.5%; Pred. No. 30; 3; Indels es 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Croizier L., Taha A., Croizier G., Lopez Ferber M.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF499596; AAM70285.1; -. GO, GO:0030528; P:transcription regulator activity; IEA. GO; GO:0045449; P:regulation of transcription; IEA. InterPro; IRR007790; LEF-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF05098; LEF-4; 1.
SEQUENCE 441 AA; 51639 MW; DC7B3982232E3550 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. Teguence 326 AA; 33269 MW; 61BC539A292B959F CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Late expression factor 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000254; CBD tungal.
InterPro; IPR00103; Glyco_hydro_61.
Pfam; PF00734; CBM 1; 1.
Pfam; PF03443; Glyco_hydro_61; 1.
PROSITE; PS00562; CBD_FUNGAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 SGSTCKVGNDYYS 323
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 SGNLFNIGNNYL 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8JRX2
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Matches
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RESULT 15 Q7WZN9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                Bacteria; ProteoDacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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EMBL, AY273871; AAP81276.1; -
InterPro; IPR008707; Neisseria PilC.
Pfan; PF05567; Neisseria PilC; 1.
SEQUENCE 1170 AA; 128118 MW; 9F4CDF6D681B62F3 CRC64;
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                                                             Last sequence update)
Last annotation update)
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Pred. No. 1.6e+02;
2; Mismatches 1;
PRT; 1170 AA.
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                                           Created)
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(TrEMBLrel. 26, I
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Best Local Similarity 70...
T; Conservative
PRELIMINARY;
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                                                                                                                                                 Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=287;
                                        01-OCT-2003
01-OCT-2003
01-MAR-2004
                                                                                                                                                                                                                                                                                    STRAIN=PA14;
                                                                                                                              Name=pilY1;
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                    6NZMLO
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us-10-614-959-13.rai

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Query Match
Best Local Similarity lv..
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-383-667-13
US-08-665-202-37
 LENGTH: 13
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                                                        October 14, 2005, 16:00:04; Search time 25.5938 Seconds (without alignments) 37.917 Million cell updates/sec
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Sequence 3
Sequence 6
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Sequence
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1: /cgn2_6/ptodaca1/iaa/5A_COMB.pep:*

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6: /cgn2_6/ptodaca1/iaa/PCTUS_COMB.pep:*
         5.1.6
Compugen Ltd.
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US-08-665-202-37

US-08-665-202-42

US-08-665-202-43

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US-08-665-202-43

US-08-983-607-35

US-09-315-574-43

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US-09-315-574-39

US-09-315-574-39

US-09-490-153-18

US-09-490-153-18

US-09-490-153-18

US-09-490-153-18

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US-09-490-153-18

US-09-315-574-5

US-09-315-574-7
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         GenCore version (c) 1993 - 2005
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                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                          1 SGSTSNIGNNYVS 13
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length: 2000000000
                                                                                          US-10-614-959-13
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Match Length
                 Copyright
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seq
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                                                                                                   Perfect score:
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Maximum DB
                                         OM protein
                                                                                                           Sequence:
                                                                                                                                                    Searched:
                                                                                                                                                                                                                                               Database
                                                         Run on:
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No.
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29 61 92.4 1111 2 US-0-65-201-6.0 Sequence 15, Appl 20 58 87.9 1111 2 US-0-65-201-6.0 Sequence 15, Appl 20 58 87.9 1112 US-0-65-201-6.0 Sequence 15, Appl 20 58 87.9 1111 1 US-0-211-551-40 Sequence 10, Appl 21 59 87.9 1111 1 US-0-211-551-40 Sequence 12, Appl 21 59 87.9 1111 1 US-0-211-551-40 Sequence 12, Appl 21 57 86.4 109 1 US-0-20-769-12 Sequence 12, Appl 21 57 86.4 109 1 US-0-10-700-12 Sequence 12, Appl 21 57 86.4 109 4 US-0-9-10-0700-12 Sequence 12, Appl 21 57 86.4 109 4 US-0-9-10-0700-12 Sequence 12, Appl 21 57 86.4 109 4 US-0-9-10-11-21 Sequence 12, Appl 21 57 86.4 109 4 US-0-9-10-11-21 Sequence 12, Appl 21 59 88.4 109 4 US-0-9-10-11-22 111 Sequence 12, Appl 21 59 88.4 109 4 US-0-9-10-11-22 111 Sequence 13, Appl 41 59 80.3 98 1 US-0-11-22-111 Sequence 13, Appl 41 59 80.3 98 1 US-0-11-22-111 Sequence 13, Appl 41 59 80.3 98 1 US-0-11-22-111 Sequence 13, Appl 41 59 80.3 98 1 US-0-11-22-111 Sequence 13, Appl 41 59 80.3 98 1 US-0-11-22-111 Sequence 13, Appl 41 59 80.3 98 1 US-0-11-22-111 Sequence 13, Appl 41 59 80.3 98 1 US-0-11-22-111 Sequence 13, Appl 42 59 80.3 98 1 US-0-11-22-111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-22-111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-22-111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-22-11-22 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-22-11-22 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-22 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-22-11-22 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-22 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-22 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-22 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-22 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-23 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-23 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-23 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-23 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-23 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-23 111 Sequence 13, Appl 44 59 80.3 98 1 US-0-11-23-11-23 11 Sequence 13, Appl 44 5
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93.9%;
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-665-202-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Schier, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to TINUER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62; DB 2; Length 98;
Pred. No. 0.007;
1; Mismatches 0; Indels
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STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/315,574
FILING DATE: 20-MAY 99
CLASSIFICATION: 530
                                  COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UW-1996
FILING DATE: 14-JUN-1996
PRIOR APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
APPLICATION NUMBER: 38 498
REFERENCE/AGENT INFORMATION:
AMME: HUNDEN: TOWNATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
CHARACTERISTI
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UN-1995
PRIOR APPLICATION DATA:
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-665-202-37
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-315-574-37
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US-08-655-202

| Bequence 36, Application US/08665202
| Patent No. 5977322
| Patent No. 5977322
| APPLICANT: Marks, James D. APPLICANT: Schier, Robert P. Ro
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Pred. No. 0.007;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                             NAME: Hunter, Tom
REGISTRATION VIMBER: 38,498
REGISTRATION VIMBER: 02307E-061411
TELECOMUNICATION INFORMATION:
TELEPRONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 377:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US 60/000,250 FILING DATE: 15-JUN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/665,202 FILING DATE: 13-JUN-1996 ATTORNEY/AGENT INFORMATION:
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RESULT 7
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                                  93.9%; Score 62; DB 2; Length 111; 92.3%; Pred. No. 0.0079; ive 1; Mismatches 0; Indels
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                                                                      23 SGSSSNIGNNYVS 35
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                                                              1 SGSTSNIGNNYVS 13
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                                                 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-36
                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                  Query Match
Best Local Similarity
Matches 12; Conserva
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Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-08-665-202-42
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RESULT 6 US-08-665-202-43

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Sequence 43, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: ADDRESSE: ADDRESS:
CITY: San Francisco
STREET: ADDRESSE: ADDRESS:
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Sequence 35, Application US/08983607
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alan Garen
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
TITLE OF INVENTION: bodies
TITLE OF INVENTION: bodies
TITLE OF INVENTION: bodies
TORRESPONDENCE: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 26 Whitney Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 62; DB 2; Length 111
Pred. No. 0.0079;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: FI-OPPY disk

MEDIUM TYPE: FI-OPPY disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFCATTON: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: Hunter. Tom
REGISTRATION NUMBER: 02307E-061410
TELERDHOME: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUINCE CHARATTERSICS:
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XY: United States of America
06520-8114
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Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide US-08-665-202-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
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Fatent No. 6512097

GENERAL INFORMATION:

APPLICANT: Schier, Nobert

TITLE OF INVENTION:

TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.

STREST: Four Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California

COUWTRY: USA

IP: 94111-4106

COMPUTER: Eloppy disk

COMPUTER: Eloppy disk

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/315,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 0.0079;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOUNCE:
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: And with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
LIBRARY: DN414 scFv antibodies obtained from
LIBRARY: fUSES fusion phage construct
CLONE: V373
FEATURE:
                                    COMPUTER: IBM PC
COMPUTER: IBM PC
SOFFWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: APPLICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1B96/01032
FILING DATE: June 20, 1996
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: WARY M. Krinsky
RECISTRATION: NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 residues
TYPE: amino acid
STRANDEDBESS: single
TOPOLOGY: linear
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 92.3
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: light chain US-08-983-607-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-09-315-574-36
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PRIOR PRICATION NUMBER: US 60/000,238

PRING DATE: 14-TUN-1995

PRING DATE: 14-TUN-1995

PRING DATE: 14-TUN-1995

PRING DATE: 14-TUN-1995

PRING THE 13-TUN-1996

PRING PRILCATION NUMBER: US 60/000,250

PRING THE 13-TUN-1996

PRING PRILCATION NUMBER: US 60/665,202

PRING THE 13-TUN-1996

PRING THE TREE THE 11 Amin to acid a stream to the total stream t
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Query Match
Best Local Similarity 92.3.
                                                                                                                                            23 SGSSSNIGNNYVS 35
                                                                                                                 1 SGSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-665-202-39
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Sequence 43, Application US/09315574

Sequence 43, Application US/09315574

Patent No. 6512097

APPLICANT: Marks, James D.

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to TITLE OF INVENTION: Tunor Antigens

NUMBER OF-SEQUENCES: 141

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                         Score 62, DB 4; Length 111;
Pred. No. 0.0079;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUMPUTAT: USA

ZIP: 94111-4106

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 13-JUN-1995
ATTONNUMBER: US 60/665,202
FILING DATE: 13-JUN-1996
ATTONNUMBER: US 60/665,202
FILING DATE: 13-JUN-1996
ATTONNUMBER: US 60/665,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C. STREET: Four Embarcadero Center, Suite 1100 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             93.9%;
92.3%;
                                                                                                                                                     LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          23 SGSSSNIGNNYVS 35
                                                                                                                                                                                                                                                                                                                                                                                               1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-315-574-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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RESULT 11
US-08-665-202-39

US-08-665-202-39

Sequence 39, Application US/08665202

Patent No. 5977322

GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert

TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: USA

COUNTRY: USA
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                                                         Gaps
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0
                    Length 111;
Score 62; DB 4; Length All Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INPORMATION:
NAME: HINDER: TORMATION:
NAME: HINDER: TORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; DB 2;
Pred. No. 0.008;
1; Mismatches
                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02307E-061410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-983-607-31
; Sequence 31, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 0230
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.9%;
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Alan Garen
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RESULT 14
US-09-315-574-39
i Sequence 39, Application US/09315574
j Fatent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
STREET: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER PAPLICATION DATA:
APPLICATION NUMBER: 20-MAY-99
CLASSIFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 14-UUN-1995
FILING DATE: 14-UUN-1995
                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT: IROCMATION:
NAME: James F. Haley, Jr., ESG.
REGISTRATION NUMBER: 27,794
CONTRACTOR NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 62; DB 3; Length 112;
Pred. No. 0.008;
                                       ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPERENCE DOCKET NUMBER: MORPHO/S
RELECOMMUNICATION INFORMATION:
TELEPHORE: (212)596-9000
TELEPKX: (212)596-9000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 92.5.
Best Local 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSSSNIGNNYVS 35
                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
      UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
                                                                                                                                                              ZIP: 10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-025-769B-18
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Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Pack, Peter
APPLICANT: 1lag, Vic
APPLICANT: Moroney, Simon
APPLICANT: Plucckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: homo sapiens (melanoma cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMBEDIATE SOURCE:
IMBEDIATE SOURCE:
LIBRARY: FUSES fusion phage construct
CLONE: V73
                                                                                                                             ADDRESSEE: and Biochemistry, Yale Unive
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZID: 06520-814
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.49 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.49 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.49 Mb diskette
COMPUTER: Mord Processing
CUMPUTER READABLE FORT
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION NUMBER: PCT/IB96/01032
FILING DATE: JUME 28, 1996
CLASSIFICATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 32423
REFERENCE/DOCKET NUMBER: 0CR-679
TELEPHONE: 203-773-1183
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 residues
STEAMEDDNESS: SINGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 93.9%;
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SGSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY: light chain US-08-983-607-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-025-769B-18
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Gaps

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           Score 62; DB 4; Length 112;
Pred. No. 0.008;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNAY ATTOLLATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REGISTRATION NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEPHONE: (202) 912-2020
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-70N-1995
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-70N-1996
ATTORNEY, AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 02307E-061411
TELEPHONE: 7576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TELENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 112 amino acids
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92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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Query Match
100.0%; Score 66; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels
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US-09-880-748-1898
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LENGTH: 240
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Sequence 1898, Ap
Sequence 24, Appl
Sequence 40, Appl
Sequence 1927, Ap
Sequence 1927, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 33, Appl
Sequence 53, Appl
Sequence 53, Appl
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                                                                                                             October 14, 2005, 16:20:10 ; Search time 92.4219 Seconds (without alignments) 58.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
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22: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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Compugen Ltd
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US-10-293-418-1898
US-10-981-692-24
US-10-981-692-40
US-09-880-748-1927
US-10-325-673-53
US-10-981-692-29
US-10-981-652-33
US-10-981-465-53
US-10-981-465-53
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                                                                                                                                                                                                                                                                                                                              1859788 seqs, 416717961 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
GenCore version
(c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB
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53, Appl
53, Appl
26, Appl
1926, Ap
1926, Ap
3241, Ap
31, Appl
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46, Appl
88, Appl
27, Appl
37, Appl
44, Appl
39, Appl
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; Sequence 1898, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT PILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PATENTIN VET: 2.0
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Sequence 1
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Sequence 1
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Sequence 6
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Sequence 4
Sequence 3
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Sequence 2
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    Sequence
US-10-981-673-53
US-10-981-691-53
US-10-981-691-53
US-10-293-418-1926
US-10-293-418-1926
US-10-293-418-1926
US-10-981-692-36
US-09-880-748-1913
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US-10-981-692-39
US-09-880-748-1618
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TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REPRENCE: PFS90B1

CURRENT APPLICATION NUMBER: US/10/981,692

CURRENT FILING DATE: 2004-11-05

PRIOR PEPLICATION NUMBER: PCT/US03/16802

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2002-05-30

NUMBER: OF SQ ID NOS: 76

SOFTWARE: PatentIn version 3.1

SEQ ID NO 40

LENGTH: 242
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Publication No. US2003005997A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-11

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239
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100.0%; Pred. No. 0.007;
rative 0; Mismatches 0;
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"Sequence 40, Application US/10981692
"Publication No. US20050163777A1
"GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: N015D10 scFv
US-10-981-692-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 SGSTSNIGNNYVS 166
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                     154 SGSTSNIGNNYVS 166
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Best Local Similarity 100.
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-880-748-1927
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Matches 13; Conserva
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US-09-880-748-1927
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US-10-981-692-33

US-10-981-692-33

Sequence 33, Application US/10981692

Publication No. US20050163777A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
FILE REFERENCE: PF590P1

CURRENT FAPLICATION NUMBER: US/10/981,692

CURRENT FILING DATE: 2004-11-05

PRIOR APPLICATION NUMBER: PCT/US03/16802

PRIOR PILING DATE: 2002-05-29

PRIOR PILING DATE: 2002-05-29

PRIOR PILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn version 3.1

SEQ ID NO 33

LENGTH: 243
                                                                          Query Match 100.0%; Score 66; DB 15; Length 243; Best Local Similarity 100.0%; Pred. No. 0.007; Matches 13; Conservative 0; Mismatches 0; Indels C
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Pred. No. 0.007;
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CTHER INFORMATION: N023E01 scFv US-10-981-692-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: N024E07 scFv
US-10-981-692-29
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
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TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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ORGANISM: Artificial sequence
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; ORGANISM: Homo sapiens
US-10-293-418-1927
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                                                                                        Sequence 53, Application US/1032673

Fublication No. US20030180296A1

GENERAL INFORMATION:

APPLICANT: Salcede et al.

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

FILE REPERENCE: PFS95

CURRENT PLING DATE: 2002-12-19

FRIOR APPLICATION NUMBER: 60/341,237

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR PLING DATE: 2002-02-04

PRIOR FILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-06-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-13

NUMBER 0F SEQ ID NOS: 72

LENGTH: 243
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Sequence 1927, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TTILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR APPLICATION NUMBER: 00/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-01-07-05-05

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16
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US-10-322-673-53
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ORGANISM: Artificial sequence
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US-10-981-673-53
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APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

CURRENT PILING DATE: 2004-11-05

PRIOR PELICATION NUMBER: 06/608,386

PRIOR FILING DATE: 2004-09-10

PRIOR FILING DATE: 2004-05-05

PRIOR FILING DATE: 2004-05-06

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-08-15

PRIOR FILING DATE: 2003-08-15

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-05-04

PRIOR FILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18
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Sequence 53, Application US/10981621

Sequence 53, Application US/10981621

GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF585P1D1

CURRENT FILING DATE: 2004-11-05

PRIOR PLING DATE: 2004-11-05

PRIOR APPLICATION NUMBER: 06/608,386

PRIOR PLING DATE: 2004-09-10

PRIOR PLING DATE: 2004-09-10

PRIOR FILING DATE: 2004-05-05

PRIOR FILING DATE: 2004-05-06

PRIOR FILING DATE: 2004-05-06

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-05-06

PRIOR PLICATION NUMBER: 60/495,140
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                                                                                                                                                                                                                           Sequence 53, Application US/10981465 Publication No. US20050214205A1 GENERAL INFORMATION:
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LENGTH: 243
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PRIOR FILING DATE: 2019-15.

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PRIOR FILING DATE: 2019-15.

PRIOR FILING DATE: 2019-16.

PRIOR FILING DATE: 2019-16.

PRIOR FILING DATE: 2019-16.

PRIOR FILING DATE: 2019-16.

PRIOR PRICATION WINERS: 6/195, 917

PRIOR APPLICATION WIN
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FEATURE:
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US-10-981-632-26
US-10-981-632-26
Sequence 26, Application US/10981692
Publication No. US2005016377A1
GENERAL INFORMATION:
TILLE REPERBUCE: PFS-90P1
TILLE REPERBUCE: PFS-90P1
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR APPLICATION NUMBER: 60/383,802
PRIOR FILING DATE: 2002-05-30
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REPRENCE: PF565P1D3
CURRENT PEPS6FD1D3
CURRENT APPLICATION NUMBER: US/10/981,691
CURRENT APPLICATION NUMBER: 60/608,386
PRIOR FILING DATE: 2004-11-05
PRIOR FILING DATE: 2004-09-10
PRIOR FILING DATE: 2004-06-05
PRIOR FILING DATE: 2004-06-05
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-08-15
PRIOR FILING DATE: 2003-08-15
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-08-15
PRIOR FILING DATE: 2002-08-15
PRIOR FILING DATE: 2002-08-15
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-13
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                        100.0%; Score 66; DB 18; Length 243; 100.0%; Pred. No. 0.007; tive 0; Mismatches 0; Indels (
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, Sequence 53, Application US/10981691

; Publication No. US20050214208A1

; GENERAL INFORMATION:
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ORGANISM: Artificial sequence
                                                                                                                                                                                   155 SGSTSNIGNNYVS 167
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Query Match
Best Local Similarity
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Best Local Similarity
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Job time : 92.4219 secs
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US-10-981-692-26
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                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
                                                PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 SGSTSNIGNNYVS 168
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NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin versic
SEQ ID NO 26
LENGTH: 244
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US-09-880-748-1926
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Best Local Similarity
Matches 13; Conserv
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US-09-880-748-1926
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GenCore version (c) 1993 - 2005
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- protein search, using sw model OM protein October 14, 2005, 15:51:19 ; Search time 53.8125 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-14 35

1 DVSKRPS 7 score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

seq length: 0 seq length: 200000000 留留 Minimum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Maximum

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A Geneseq 16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	072 Anti-fact	338 Vlambda g	544 Anti-adip	060 Human ant		•	•		_				416 Anti-huma	BCFV 7	Human	084 Human dia		714 Single ch		_		317 Neurokini		_	
	Desci	Aay79072	Adj 80338	Aau02544	Aay96060	Aau 02558	Aau02612	Aau02627	Aau02629	Aaw19883	Aau02542	Aau02551	Aau02585	Adk17416	Adg42838	Abm8	Abm85084	Abp4	Adg96714	Abp46044	Adg96871	Adg34301	Adg34317	Abp45916	Adg96743	Adg34310
	ID	AAY79072	ADJ80338	AAU02544	AAY96060	AAU02558	AAU02612	AAU02627	AAU02629	AAW19883	AAU02542	AAU02551	AAU02585	ADK17416	ADG42838	ABM85072	ABM85084	ABP45887	ADG96714	ABP46044	ADG96871	ADG34301	ADG34317	ABP45916	ADG96743	ADG34310
	DB	m	7	4	m	4	4	4	4	7	4	4	4	7	œ	œ	œ	S	7	S	7	œ	80	Ŋ	7	80
	Query Match Length DB	7	66	109	110	110	110	110	110	111	111	111	111	111	111	214	236	240	240	241	241	242	242	243	243	243
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35								35		35
	Result No.	1	8	m	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Adg34306 Neurokini Abg45915 Human BLy Adg96742 Single ch Adg98057 TNF proli Adg34318 Neurokine Adg34313 Neurokini Abp45802 Human BLy Adg96739 Single ch Adg96739 Single ch Adg96739 Single ch Adg96732 Single ch Adg8722 Human BLy Abp45674 Human BLy Abp45677 Human BLy Abp45677 Human BLy Abp45677 Human BLy Abp45917 Human BLy Abp45917 Human BLy Abp4598 Human BLy	
ADG34306 ADG34303 ABR45315 ADG96742 ADG96742 ADG34308 ADG34308 ADG34308 ADG34308 ADG34308 ADG96729 ABR45972 ABR45671 ABR45671 ABR45671 ABR45671 ABR45671 ABR45917 ABR45917 ABR45917 ABR45917 ABR45917	
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
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## ALIGNMENTS

Complementarity determining region 2; CDR2; antibody; Gla domain; factor IX/IXIs, blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina, post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. Anti-factor IX/IXa antibody L chain V domain CDR2 amino acid sequence. AAY79072 standard; peptide; 7 AA. (first entry) 12-JUN-2000 AAY79072; 

Homo sapiens.

WO200012562-A1

09-MAR-2000.

99WO-US019453. 26-AUG-1999; 98US-0098233P. 99US-0122767P. 28-AUG-1998;

03-MAR-1999;

(GETH ) GENENTECH INC.

Kirchhofer D; Devaux B, Eaton DL, Hass PE, Judice JK, Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 2 (CDR2) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood cogulation parhways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (1) providing an initial antibody having epecificity for a traget; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the region of the first component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from a traget species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component of the variable region which is different than the first component, the second component selected from the group consisting of FR1, FR2, FR3 and FR4; (vi) comparing the sequence of the second component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from the target species; (viii) selecting a sequence from the database of antibody to the second component and which is from a different ceptody than the selected antibody; and (ix) operatively linking the
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the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary artery bypass graft (the production of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hybrid antibody; antibody; framework region; homology; immunogenicity.
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                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 35; DB 3; L
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
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Best Local Similarity 100.000
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                                                                                                                                                                                                                                                                                                                                                  Sequence 7 AA;
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ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies may be labeled with a
dipocytes can be used to activate the immune system to destroy the cells
of complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte such as mathodies can be used as an alternative means of treatment for obese
the antibodies can be used as an alternative means of treatment for obese
can be used as an alternative means of treatment for obese
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selected framework sequences to one or more complementarity determining regions (CDRs) of the initial antibody to produce a hybrid antibody or hybrid antibody fragment. The method is useful for producing a hybrid antibody or hybrid antibody fragment (claimed). The antibody and fragments are useful for therapeutic and diagnostic purposes. The method uses entire framework regions from a single antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that are highly homologous and exhibit reduced immunogenicity while maintaining an optimum binding profile. This sequence represents the amino acid sequence of an antibody from the Vlambda gene locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 7
100.0%; Pred. No. 5.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02544 standard; protein; 109 AA.
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                                                                                                                                                                                                                                 Sequence 99 AA;
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AAU02558;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Making antibodies (e.g. anti-decay accelerating factor antibody) for diagnosing or treating e.g. lung cancer comprises identifying an antigen that is differentially expressed on the surface of two or more distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of the light chain variable region (VL) of the anti-decay accelerating factor (DAP) human antibody LU30. The VH region is given in AAY06063. LU30 has a binding affinity (Kd) for DAF of about 13 nM. It was produced using a novel method for making antibodies which can be used for cancer diagnosis or therapy. The method comprises:
                                                                                         Gaps
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                    LU30; human; antibody; VL domain; decay accelerating factor; DAF; phage display; subtractive panning; lung cancer; lung carcinoma; lung adenocarcinoma; therapy; diagnosis.
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/label= CDRIII
/note= "complementarity determining region III"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "complementarity determining region II"
                                                                                                                                                                                                                                                                                                                                                                                            23. .36
/label= CDRI
/note= "complementarity determining region
                                                              4; Length 109;
                                                                                                                                                                                                                                                                               Human anti-DAF antibody LU30 light chain variable region.
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te= "hypervariable loop residues'
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ce= "hypervariable loop region"
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                                                             100.0%; Score 35; 100.0%; Pred. No. 6
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                                                                                                                                                                                                    AAY96060 standard; protein; 110 AA.
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/label= CDRII
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Best Local Similarity luv...
7; Conservative
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                                       Sequence 109
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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(a) binding an antibody phage from a naive antibody phage library to a live cancer cell; (b) selecting an antibody phage or antibody which binds selectively to the live cancer cell; and (c) identifying an antibody which the antibody phage or antibody binds. To obtain LU30, a human scrv library was used to search for tumour-associated antigens by panning the lung adenocarcinoma cell line 1264, and counter-selecting with a non-tumour bronchial spithelial cell line, BEAS-2B. The invention also describes a method for identifying an antigen which is differentially expressed on the surface of 2 or more distinct cell populations. The anti-DAF human antibody, or a composition comprising the antibody, is useful for in vivo cancer disgnosis or therapy. In particular, the antibody is useful for in vivo cancer disgnosis or therapy. In particular, the antibody is useful for an or confermed lung cancer, e.g. small-cell lung cancer, non-small cell lung cancer, large cell lung carcinoma, lung adenocarcinoma, or squamous cell lung carcinoma (all claimed)
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Best Local Similarity 100.
Matches 7; Conservative
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N-PSDB; AAS03458.
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DB 4; Length 110;

Query Match

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and heavy chain complementarity determining regions (CDR) of the antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a confidence in methods of disquosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies con fulfillerent types of fat deposits can also be produced e.g. intra-
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presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
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                                                                                                                                                                   100.0%; Score 35; DB 4; Length 110; 100.0%; Pred. No. 6.1; ive 0; Mismatches 0; Indels
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abdominal fat associated with heart disease

Sequence 110 AA;

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requences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for abdominal fat associated with heart disease
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heart disease; complementarity determining region; CDR.
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100.0%; Score 35;
100.0%; Pred. No. (
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                                7: Conservative
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N-PSDB; AAS03527.
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AAU02629;

RESULT 8

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This polypeptide sequence comprises the light chain variable region (VL) of human carcinoembryonic antigen (hCEA) specific antibodies CEA1, CEA2 and CEA3. VH (AAT72126-33) and VL (AAT7213-35) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see AAM19876-85). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10-8 M, is non- cross-reactive with human liver cells, and preferentially binds to the A3-83 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL variants. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer.
                                                                              Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
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/label= CDR1
/note= "complementarity determining region 1"
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/note= "complementarity determining region 3"
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                                         CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.
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/label= CDR2
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07-DEC-1997 (first entry)
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N-PSDB; AAT72133.
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Best Local Similarity
7; Conserve
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23-MAY-1996;
11-OCT-1996;
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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
consisty related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the far mass of an obese patient or the antibody
can be used as a therapeutic treaff. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
adipocytes as a readiolabel, fluorescent or chemical group and
cused in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
considers other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                 AAU02629 standard; protein; 110 AA.
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N-PSDB; AAS03451.
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                                               WO200127279-A1
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Homo sapiens.
                                                                                                                                                                                                 12-OCT-1999;
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                                                                                              19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU02585;
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AAU02585
X L X D X L X S X M X X D X L X Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
cinvention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
cobesity related diseases. The antibodies binding specifically to
can be used as a therspeutic (teelf. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
cused in methods of diagnosis in human subjects e.g. to determine the
cused in methods of diagnosis in human subjects e.g. to determine the
cused in methods or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
cor the antibodies can be used as an alternative means of treatment for obese
cor patients other than undergoing surgery to remove excess fat. Antibodies
cor different types of fat deposits can also be produced e.g. intra-
cor additional fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                   Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 35; DB 4; Length 111; 100.0%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-adipocyte monoclonal antibody light chain, FAT 37.
                                                                      Anti-adipocyte monoclonal antibody light chain, FAT 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 118-119; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU02551 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                 11-OCT-2000; 2000WO-GB003900
                                                                                                                                                                                                                                                                                                                                                                                                  99US-0158812P
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                    29-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Main SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-282031/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 DVSKRPS 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS03442
                                                                                                                                                                                                                                                   WO200127279-A1.
                                                                                                                                                                                                 Homo sapiens.
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diseases.

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Gaps

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fat;

AAU02551;

AAU02551 ID AAU0 XX AC AAU0 XX DT 29-1 XX DE ANUX XX ANUX XX ANUX

RESULT 11

Query Match

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WPI; 2003-731501/69.
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(ZHUL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
ADG42838
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                                                                                                                                                                                             AAU02501-AAU02615, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic Itself. Antibodies binding specifically to adjocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the
                                                                                                                                                                                                                                                                                                                                                                       The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                              presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample.
                                                                                                                    Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-HIV; cytostatic; virucide; single chain antibody; antibody; yeast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 35; DB 4; Length 111; 100.0%; Pred. No. 6.1; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-human CXCR4 loop 6 ScFv antibody Vl region.
                           (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK17416 standard; protein; 111 AA.
                                                    Vaughan TJ;
                                                                                                                                                                        Claim 1; Page 146; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2002; 2002US-00071866.
08-FEB-2002; 2002US-00072031.
25-APR-2002; 2002US-00133978.
 99US-0158812P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENETASTIX CORP.
                                                    Main SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pauling MH,
                                                                              WPI; 2001-282031/29.
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| DVSKRPS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DVSKRPS 7
                                                                                           N-PSDB; AAS03485
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 111 AA;
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12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV; cancer;
                                                    Edwards BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                               diseases
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Matches
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The invention relates to a method of selecting a single chain antibody (scPv) against a peptide target in a yeast by expressing a library of scPv) against a peptide target in a yeast by expressing a library of scPv fusion proteins in yeast cells expressing the scPv fusion proteins brotein.

In the yeast cells expressing the scPv fusion proteins having either the DNA binding domain or the activation domain of the transcription cartivator which is not comprised in the scPv fusion proteins, and a ctarget peptide, and selecting those yeast cells in which a reporter gene is expressed. Each scPv fusion protein comprises either an activation domain or a DNA binding domain of a transcription activator and a scPv having a heavy chain of a variable region (VH) of antibody whose sequence varies within the library, a light chain of a variable region (VH) of antibody whose sequence varies within the library independently of the CC antibody whose sequence varies within the library independently of the CC and a linker peptide which links the VH and VL. The expression of the creporter gene is activated by a reconstituted transcriptional activator corresponds to the scPv fusion protein to the target fusion creporter. The methods and compositions of the protein. The methods and compositions of the present invention are useful corresponds to the VI region of an anti-human CXCR4 loop 6 antibody gene corresponds to the VI region of an anti-human cXCR4 loop 6 antibody gene corresponds.
Selecting an scFv against a peptide target by expressing a target fusion procein having a bNA binding domain or activation domain of a transcription activator, useful for diagnosing, preventing and/or treating HIV infection and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV infection; HIV type 1; HIV type 2; cancer; breast; prostate; liver; renal; lung; skin; ovarian; cervical; brain; thyroid; stomach; colon; lymphoma; leukaemia; pancreas; chemokine receptor; antibody.
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                                                                                                                                            Claim 123; SEQ ID NO 61; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scFv Ab124 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG42838 standard; protein; 111 AA.
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08-FEB-2002; 2002US-00072301.
25-APR-2002; 2002US-00133978.
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Best Local Similarity luv...
7; Conservative
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PAULING M H.
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                                                                                                 The invention relates to an antibody that binds to loop 6 of human chemokine receptor (CKCR4). The antibody is useful in the treatment or prevention of HIV infection (e.g. HIV type 1 and HIV type 2) and cancer of (e.g. breast, prostate, liver, renal, lung, skin, ovarian, cervical, brain, thyroid, stomach, colon, lymphoma, leukaemia and pancreas cancer cells), for screening drugs, for diagnoshing disease or condition associated with interaction with chemokine receptor. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Allus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panesar SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lugace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES,
Ru Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
Patury S, Shi X, Suarez CJ;
                           Antibody binding loop of human chemokine receptor useful for the treatment of HIV infection and cancer.
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                                                                                                                                                                                                                                                                     100.0%; Score 35; DB 8; Length 111; 100.0%; Pred. No. 6.1;
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                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                       Claim 6; SEQ ID NO 61; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM85072 standard; protein; 214 AA.
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12-SEP-2002; 2002US-0410260P.
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                                                                                                                                                                                                                                                                                                                                 1 DVSKRPS 7
                                                                                                                                                                                                                                                                                    Local Similarity
N-PSDB; ADG42836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ACN43724
                                                                                                                                                                                                                                         Sequence 111 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004023973-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Patury S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM85072;
                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification,  ${\bf A}$ 

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                            diagnostic and therapeutic polynuclectides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorder, endocrine disorder, endocrine disorder, neurological disorder, gastrointestinal disorder, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gone therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from NIPO at www.wipo.int/pct/en/sequences/listing.htm
polynucleotide of the invention may have a use in gene therapy. The human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVSKRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 214 AA;
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Search completed: October 14, 2005, 16:12:42 Job time : 54.8125 secs

Sun Oct 16 15:00:25 2005

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

October 14, 2005, 16:02:59; Search time 9.73438 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-14 35 Title: Perfect score:

1 DVSKRPS 7 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

35 100	Query Match 1	Length	DB	a	Description
2			1 :	836067	The Table of the Control of the Cont
	97.1	646	10	G85056	bable r
91	4.	9	N	A24626	Îg lambda chain V-
91	4.	103	~	A38923	AL type amyloid fi
	4.	111	Н	L2HUTR	Ig lambda chain V-
	91.4	423	7	F64690	
	9.88	110	N	S51149	_
œ	9.	111	Н	L2HUWN	lambda
œ	9.	111	~	S36281	Ig lambda chain V
œ	5.7	112	7	S31515	
	. 7	112	~	S44105	Ig lambda chain V-
	. 7	416	~	S26836	type II site-speci
	0.	74	~	AH2642	hypothetical prote
	ο.	88	~	A97425	
	σ.	337		E70191	conserved hypothet
	6.	377	~	A32548	
	82.9	404	~	T00750	probable protein p
	ο.	685	N	T21466	
	6	690	N	T21806	hypothetical prote
	σ.	735	N	T00850	probable receptor-
	6	972	N	H84903	hypothetical prote
	6.	1033	~	T37715	actin-interacting
29 82.	6.	1077	N	T21800	hypothetical prote
	6	1245	~	G84897	hypothetical prote
	0.0	91	~	T09711	ADP, ATP carrier pr
	0.	111	Н	L2HUMC	Ig lambda chain V-
28 80	0.	189	~	AE1316	
28 80	٠	189	~	AE1688	n.
28 80	0.	235	~	825759	Ig lambda chain -

ig lambda chain - 60s ribosomal prot hypothetical prote	hypothetical prote probable lipoprote hypothetical prote	mutants block spor thioredoxin-disulf thioredoxin reduct	thioredoxin reduct familial Alzheimer SRPM54 protein - M	hypothetical prote gene 12 protein - 4-hydroxybutyryl-C	pseudolysin (EC 3.
S14675 T40075 A64624	D71891 A82017 AE0243	E83999 B97777 D71703	G87604 S65358 S35481	T40769 Z2BPC2 F90422	HYBSPA
000	0 00	0 0 0	000	242	-
235	300 301	309 310 310	348 440 447	452 458 463	498
80.0	0000	80.08 80.00	80.0 80.0	0.00	80.0
7 7 7	9889	78 78 78 78	7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	7 7 7	78
330	1 60 60 1 60 44 73	36 37 38	39 40 41	4. 4. 4 G & 4	45

# ALIGNMENTS

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CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens
CiDacession: S36057
Riwilliams, S.C.
Submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Reference number: S36046
A;Reference number: S36057
A;Referen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:222198; NID:9312319; PIDN:CAA80208.1; PID:9312320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>
```

ö Query Match
100.0%; Score 35; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels

ö

Gaps

RESULT 2

probable receptor-like protein kinase [imported] - Arabidopsis thaliana Cisbecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
C;Accession: G85056
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: G85056
A;Status: preliminary
A;Accession: DNA
A; Passiduse: 15-646
A; Passiduse: 15-6466
A; Passiduse: 15-64666
A; Passiduse: 15-64666
A; Passiduse: 15-64666
A; Passiduse: 15-64666
A; Passiduse: 15-646

A, Cross-references: UNIPROT: Q9XEC7; GB:NC_001268; NID: g7267207; PIDN: CAB77918.1; GSPDB:G C; Genetics:

Length 646; A;Gene: AT4g04500 A;Map position: 4 C;Superfamily: protein kinase homology

Gaps ; 0 0; Indels Query Match 97.1%; Score 34; DB 2; Best Local Similarity 85.7%; Pred. No. 12; Matches 6; Conservative 1; Mismatches (

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1 DVSKRPS 7

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A.Cross-references: GDB:119342; OMIM:147240
A.Gross-references: GDB:119342; OMIM:147240
A.Map position: 22q11.2-22q11.2
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap to complexe; An immunoglobulin heterotetramer subunit sand is a second into lact of cysuperfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: blocked amino end; heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>
F:17-92/Domain: immunoglobulin homology <IMM>
F:17-93/Domain: an immunoglobulin homology of (GIN) (probably pyrrolidone carboxylic acid) #status F:22-90/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type IIS restriction enzyme R protein - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Species: Helicobacter pylori

C;Species: Helicobacter pylori

C;Species: Helicobacter pylori

C;Accession: F64690

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Staton, G.G.; Fleischmann, R.D.

Reterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKennc, Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A;Atchescan and a sequence of the gastric pathogen Helicobacter pylori.

A;Accession: F64690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:025919; GB:AE000637; GB:AE000511; NID:92314536; PIDN:AAD0841
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C;Speciés: Hown sapiens (man)
C;Date: O'T-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S51149
R;de Kruif, J.; Boel, E.; Logtenberg, T.
R;de Kruif, J.; Boel, E.; Logtenberg, T.
A;Description: Selection and application of human SCFV antibody fragments from a semi-sy A;Reference number: S51147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                91.4%; Score 32; DB 1; Length 111; 85.7%; Pred. No. 5.9; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 2; Length 423;
Pred. No. 23;
1; Mismatches 0; Indels
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A;Residues: 1-110 <DEK>
A;Cross-references: BMBL:X83712
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;13-90/Domain: immunoglobulin homology <IMM>
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85.7%; Pred. No. 9.8;
iive 1; Mismatches
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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52 DVTKRPS 58
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A; Status: preliminary
A; Molecule type: mRNA
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B. Bulitz, M.; Linke, R.P.
Balochem. Biophys. Res. Commun. 194, 1427-1434, 1993
B. Biochem. Biophys. Res. Commun. 194, 1427-1434, 1993
A.Title: The precursor molecule of a V-lambda II-immunoglobulin light chain-derived amyla A. Reference number: A38923; MUID: 93356823; PMID: 8352801
A. Accession: A38923
A. A. Accession: A38923
A. A. Residues: 1-95;96-103 «EUL»
C. Comment: This protein is derived from an immunoglobulin light chain of lambda type. C. Superfamily: immunoglobulin vegion; immunoglobulin homology
C. Keywords: amyloid; immunoglobulin
F:1-58/Product: AL type amyloid fibril protein #status predicted «MAT»
F:7-83/Domain: immunoglobulin homology < IMM»
                                                                                                                                                                                                                                                         Chaccession: A24626
R;Eulitz, M.; Linke, R.
Biol. Chem. Hoppe-Seyler 366, 907-915, 1985
A;Title: Amyloid fibrils derived from V-region together with C-region fragments from a ...
A;Reference number: A24626, MUID:86077295; PMID:3935132
A;Accession: A24626
A;Molecule type: protein
A;Residues: 1-60 < EUL.>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tambda chain V-II region (Tro) - human (tentative sequence)

Cispeciae: Homo sapiens (man)

Cispeciae: Homo sapiens (man)

Cispeciae: Homo sapiens (man)

Cispeciae: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004

Cispeciae: A01973

Rischolz, R.; Yang, C.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 360, 1903-1918, 1979

A; Reference number: A01973; MUD:80114123; PMID:118915

A; Accession: A01973

C; Comment: This chain was isolated from a myeloma protein.

C; Comment: This chain was isolated from a myeloma protein.
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                                                                                                                                                                  Ig lambda chain V-II region (Har) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Species: Homo sapiens (man)
C,Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 60;
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Pred. No. 3.1;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
          DISKRPS 612
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submitted to the EMBL Data Library, January 1993
A;Description: V-lambda-2 gene sequence of a high affinity anti-idiotypic IgM antibody f
A;Reference number: S31515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: 844105
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Abeaription: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Accession: $44105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule_type: DNA
A;Residues: 1-416 <BOC>
A;Cross-references: UNIPROT:P23191; EMBL:X56977; NID:g44180; PIDN:CAA40298.1; PID:g44182
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R,Bocklage, H.; Heeger, K.; Mueller-Hill, B.
Nucleic Acids Res. 19, 1007-1013, 1991
A,Title: Cloning and characterization of the MboII restriction-modification system.
A,Reference number: S26835; MUID:91212177; PMID:2020540
A,Accession: S26836
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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C;Date: 03-Mar-1994 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:231388; NID:g472959; PIDN:CAAB3263.1; PID:g940517
Subperfamily: immunoglobulin V region; immunoglobulin homology
C;Ksywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                               A;Cross-references: EMBL:219546; NID:g33754; PIDN:CAA79606.1; PID:g33755 Cs. Csuperfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:15-92/Domain: immunoglobulin homology <IMM>
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Pred. No. 64;
1; Mismatches
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Pred. No. 17;
0; Mismatches
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Pred. No. 17;
0; Mismatches
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Ig lambda chain V-J region - human
                                                                                                                                                                                                                                                                                                                                                                                               h 85.7%;
Similarity 85.7%;
6; Conservative
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Similarity 85.7%;
6; Conservative
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5; Conservative
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
                                                                                              A, Accession: 831515
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-112 < VAN>
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A;Molecule type: DNA
A;Residues: 1-112 <HAW>
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Best Local Similarity
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                                                                                                            Iglambda chain V-II region (Win) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: A01978
R;Chen, B.L.; Chiu, Y.Y.H.; Humphrey, R.L.; Poljak, R.J.
Biochim. Biophys. Acts 537, 9-21, 1978
A;Tille: Anino acid sequence of the human myeloma lambda chain Win.
A;Reference number: A01978; MUID:79062503; PMID:102365
A;Accession: A01978
A;Rolecule type: protein
A;Residues: 1-111 cCHB>
A;Residues: 1-111 cCHB>
A;Residues: 1-111 cCHB>
A;Comment: This is a Bence Jones protein.
C;Genetics: GDB:119342; OMIM:147240
A;Gene: GDB:119342; OMIM:147240
A;
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836281
Ig lambda chain V region (clone alpha-FOG1-A3) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 103-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C; Accession: S36281
R; Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A; Title: Human anti-self antibodies with high specificity from phage display libraries.
A; Reference number: S36286; MulD:93178448; PMID:7679990
A; Accession: S36281
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-111 -GRIS
A; Cross references: EMBL:218823; NID:g33414; PIDN:CAA79275.1; PID:g939907
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-92/Domain: immunoglobulin homology <INM>
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831515
Glambda chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31515
R;van der Heijden, R.W.J.; Uytdehaag, F.G.C.M.; Osterhaus, A.D.M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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85.7%; Pred. No. 9.9;
ive 1; Mismatches 0; Indels
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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DVDKRPS 58
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: ABS577; MUD:21608550; PMID:11743193
A,Reference number: ABS577; MUD:21608550; PMID:11743193
A,Reference preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-74 «KUR»
A,R
                                                                                                                                                C;Accession: AH2642
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rigodoner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
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C;Genetics:
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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
hypothetical protein Atu0540 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whi son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vug; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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Pred. No. 19;
1; Mismatches 1; Indels
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A,Map position: circular chromosome
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A,Gene: Atu0540
A,Map position: circular chromosome
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.49
Matches 5; Conservative
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A;Molecule type: DNA
A;Residues: 1-88 <KUR>
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Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Fitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: E70191
A;Accession: E70191
A;Accession: E70191
A;Residues: J-337 <KLE>
A;Residues: J-337 <KLE>
A;Residues: J-337 <KLE>
A;Residues: UNB</br/>
A;Residues: UNB:QSECTER (B:AE001173; GB:AE000783; NID:g2688665; PIDN:AAC6708)
A;Experimental source: strain B31
C;Superfamily: translation factor, SUA5 type
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Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches
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141 NISKRPS 147
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PRELIMINARY;
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                                                                            October 14, 2005, 15:51:44; Search time 46.5938 Seconds (without alignments) 76.932 Million cell updates/sec
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Q784h3
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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06 PSS3
09 BTM2
11 70
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LV21 HUMAN
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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O9dbj2 mus musculu 014523 homo sapien 080080 mus musculu 06d017 erwinia car 06ddp4 leifsonia x 06lwq4 methanococc 064qq1 bacteroides 088x99 drosophila 09vn46 drosophila 06vey3 vitis vinif 08uhw8 agrobacteri 06lk05 photobacteri 06lk05 protobacteri 06lk05 erwinia car	3
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RESULT 1

GONECT CONTINUARY, PRT, 646 AA.

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GONECT CONTINUARY, PRT, 646 AA.

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casrainci P., Fornet T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Althing M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
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STRAIN-26695 / ATCC 700392;
MEDILINE-9794467; PubMed-9252185; DOI=10.1038/41483;
Tomb J.-P., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Pleisenmann R.D., Ketchum K.A., Klenk H.-P., Gill S.K.,
Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 2; Length 236;
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030983; AAH30983.1; -.
HSSP; P01709; 1A8J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 236 AA; 25021 MW; 4A07BEF60A5FD465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 26, Last annotation update)
Type IIS restriction enzyme R protein (MBOIIR).
OrderedLocusNames=HP1366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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INCEPPO, IPR001359; IG.
INCEPPO, IPR00110; IG-11ke.
INCEPPO, IPR001359; IG_0.
INCEPPO, IPR001359; IG_0.
INCEPPO, IPR001359; IG_0.
INCEPPO, IPR001359; IG_0.
INCEPPO, IRR01359; IG_0.
INCEPPO, IRR014, IG_0.
INCEPPO, IRR01, IRR
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                       DB 2; Length 646;
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By similarity.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Price protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-JUL-2004 (Rel. 44, Last annotation update)
1g lambda chain V-II region TRO.
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1; Mismatches
                                              69
                    Score 34;
Pred. No.
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
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05-JUL-2004 (TrEMBLrel. 27, C;
05-JUL-2004 (TrEMBLrel. 27, L;
05-JUL-2004 (TrEMBLrel. 27, L;
Hypothetical protein.
Homo sapiens (Human).
                    97.1%;
85.7%;
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                                            Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6, Conservative
                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                      |:|||||
606 DISKRPS 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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|DVTKRPS 58
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                  LV2D HUMAN
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SEQUENCE
                       Query Match
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LV2D_HUMAN
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1. Hischim. Biophys. Acta 537:9-21 (1978).

2. SIMILARITY: Contains 1 immunoglobulin-like domain. PIRSP; PO1709; L2HUMN.

3. RAPP: PO1709; L2HUMN.

3. RAPP: PO1709; L2HUMN.

3. RO; G0:0005576; C:extracellular; NAS.

40; G0:0005576; C:extracellular; NAS.

50; G0:0005955; P:immune response; NAS.

3. Rappose: RR G0:0005956; P:immune response; NAS.

3. Rappose: RR G0:0005965; P:immune response; NAS.
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               Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weldman J.F., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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By similarity.
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                                                                                                                                                                                                                                                                                                                                                                   423 AA; 50047 MW; 9086E51C8FE4E58E CRC64;
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PROSITE; PS50835; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing;
Immunoglobulin V region; Pyrrolidone carboxylic acid.
Ignunoglobulin V region; Pyrrolidone carboxylic acid.
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21-JUL-1986 (Rel. 01, Last sequence update)
25-JUL-2004 (Rel. 44, Last annotation update)
19 lambda chain V-II region WIN.
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                                                                                                                                                               pylori.";
Nature 388:539-547(1997).
EMBL: AR000637; AAD08410.1; -.
PIR; F64690; F64690.
                                                                                                                                                                                                                                                                                      InterPro; IPR003615; HNH nuc.
SMART; SM00507; HNHc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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71 DMSKRPS 77
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52 DVDKRPS 58
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Best Local Similarity
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                            Complete proteome.
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LV2I_HUMAN
ID _LV2I_HUMAN
AC P01712;
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Galagan J.B., Calvo S.E., Borkovich K.A., Selker B.U., Read N.D., Adalagan J.B., Calvo S.E., Borkovich K.A., Selker B.U., Read N.D., Adalagan J.B., Calvo S.E., Borkovich K.A., Selker B.U., Ratzhudh W., Mal L.-J., Smirnov S., Purcell S., Rehman B., Bikins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Schulte U., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Rothe G.O., Jedd G., Mewes W., Staben C., Marcotte B., Greenberg D., And Roy A., Foley K., Naylor J., Rhomann N., Barrett R., Greenberg D., Krystoffowa S., Ramussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arstoffowa S., Ramussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arstoffowa S., Ramussen C., Metzenberg R.L., Perkins D.D., Kroken S., Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Narden D., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander B.S., Nusbaum C., Birren B.; The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                          DOI=10.1128/JB.185.18.5591-5601.2003;
Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
Dewhirst F.B., Fraser C.M.;
"Complete genome sequence of the oral pathogenic bacterium
Porphyromonas gingivalis strain W83.";
BMEL, AROITI76; AAQ66466.1;
TIGR; PG1409;
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                     Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.6%; Score 31; DB 2; Length 130; 71.4%; Pred. No. 63; ative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome; Hypothetical protein.
SEQUENCE 130 AA; 14455 MW; 3F2E1F64F23E5805 CRC64;
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Last annotation update)
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Last annotation update)
130 AA
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                                                Created)
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PRT;
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MEDLINE=22829867; PubMed=12949112;
                                                                                                                                                                                                                          Porphyromonadaceae; Porphyromonas.
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                                             01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                  OrderedLocusNames=PG1409;
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PRELIMINARY;
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Name=NCU02220.1;
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107 DISRRPS 113
                                                                                                                        Hypothetical protein
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STEAIN-TCH46;
Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
"Genomic analysis of Bacteroides fragilis reveals extensive DNA
inversions regulating cell surface adaptation.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
EMBL; AP006841; BAD48181.1; -.
SEQUENCE 402 AA; 45596 MW; 2D56A6DAF87797CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MA-4680;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M.; Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                 Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
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                                                                                                                                                                                                                                                                                                                       Length 402;
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100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0; Indels
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InterPro; IPR001128; Cytochrome_P450.
PRINTS; PR00359; BP450.
PRINTS; PR00366; CYTOCHROME_P450; UNKNOWN 1.
Complete proteome; Heme; Mondoxygenase; Oxidoreductase.
SEQUENCE 486 AA; 53354 MW; A728B74F6592E265 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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Predicted nucleoside-diphosphate sugar epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.6%; Score 31; DB 2; I
85.7%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative cytochrome P450.
Name=cyp24; OrderedLocusNames=SAV6706;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MA-4680;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity الاست
نام 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                 Bacteroides fragilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         348 DVSKRP 353
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Best Local Similarity
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SEQUENCE FROM N.A.
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                 ORFNames=BF1430;
                                                                                             NCBI_TaxID=817
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Q828G3
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               EMBL; AABX01000366; EAA30397.1; -. GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA. GO; GO:0015035; F:protein disulfide oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDILINE=22943235; PubMed=14580944; DOI=10.1016/S0306-4522(03)00566-9;
Kucenas S., Li Z., Cox J.A., Egan T.M., Voigt M.M.;
"Molecular characterization of the zebrafish P2X receptor subunit gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY292650; AAQ21195.1; -...
ZPIN; ZDB-GENEL-030319-2; p2rx2.
ZPIN; ZDB-GENEL-030319-2; p2rx2.
GO; GO:0005503; C:light-harvesting complex (sensu Viridiplantae); IEA.
GO; GO:0005216; F:ATP binding; IEA.
GO; GO:0005216; F:ATP binding; IEA.
GO; GO:0016978; F:Inpoate-protein ligase B activity; IEA.
GO; GO:0006811; F:ecceptor activity; IEA.
GO; GO:0006691; F:ecceptor activity; IEA.
GO; GO:0006691; P:energy pathways; IEA.
GO; GO:0006811; P:ion transport; IEA.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                         2; Length 233;
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                                                                                                                                                                                       Query Match 88.6%; Score 31; DB 2; Length 233
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels
                                                                 InterPro; IRR01833; DSBA.
InterPro; IRR010986; DsbA_insertion.
Pfam; PF01323; DSBA; 1.
Hypochetical protein:
SEQUENCE 233 AA; 25367 MW; 50B8F4A369168929 CRC64;
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Last sequence update)
Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ATP-gated ionotropic P2X receptor subunit 2.
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                                                                                                                                                                                                                                                                                                                                                                                                     400 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=p2rx2; Synonyms=p2xr2;
Brachydanio rerio (Zebrafish) (Danio rerio)
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Interpro; IPR001429; P2X_receptor.
Pfam; PF00864; P2X_receptor; 1.
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Matches 6; Conservative
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222 DVSERPS 228
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25-OCT-2004 (
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Q64WES

RESULT 9

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Q64WE5

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AGD; ABL133C;
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Galagan J.B., Calvo S.B., Borkovich K.A., Selker B.U., Read N.D., Adfe D., FitzHugh W., Mal L.-J., Smirnov S., Purcell S., Rehman B., Blkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Belkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Oui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Schlitch G.P., Kinsey J.A., Braun B.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Ramal M., Kamysselsis M., Maucell E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macine G., Catcheside D., Li W., Perkins D.D., Kroken S., Aramayo R., Arden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freiteg M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa."; Nature 0:0-0(2003).
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Pubbled=14665450; DOI=10.1128/EC.2.6.1151-1161.2003;
Catlett N.L., Yoder O.C., Turgeon B.G.;
"Whole-genome analysis of two-component signal transduction genes in
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurospora crassa.
Bukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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Cochliobolus heterostrophus (Drechslera maydis).
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
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Indels
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EMBL; AABX01000022; EAA35484.1; -.
SEQUENCE 728 AA; 79550 MW; 05A688EBD3850B79 CRC64;
                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                       728 AA.
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1; Mismatches
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Matches 6; Conservative
6; Conservative
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                                                             1 DVSKRPS 7
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Name=NCU00559.1;
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Q7SF90
Matches
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ELWARTYCE CG11 2:1151-1161 (2003).

STATILARITY: Contains 1 histidine kinase domain.

STATILARITY: STATE binding; IEA.

STATILARITY: STATILARITY: STATE binding; IEA.

STATILARITY: STATILARITY: STATE binding ATPASE.

INTERPRO; IPRO01561; His Kinase.

INTERPRO; IPRO01789; Response reg.

INTERPRO; IPRO01789; Response reg.

INTERPRO; IPRO01789; Response reg.

INTERPRO; IPRO01789; Response reg.

STATE PRO0518; HARPASE.

STATE PRO0518; HARPASE.

STATE PRO0518; HARPASE.

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STRAIN=ATCC 10895;
Voegell S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T.,
Philippsen P.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AR016815; AAS50638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 85.7%; Pred. No. 9.6e+02; 6; Conservative 1; Mismatches 0; Indels
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85.7%; Pred. No. 6.9e+02;
ative 0; Mismatches 1; Indels
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PRODOM; PD000039; Response_reg; 1.

SMART; SM0038; HarRasis c; 1.

SMART; SM00448; REC; 1.

PROSITE; PS50109; HIS KIN; 1.

PROSITE; PS50109; HIS KIN; 1.

SEQUENCE 1292 AA; 144730 MW; 57010F00069FF49B CRC64;
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Saccharomycetales; Saccharomycetaceae; Eremothecium, NCBI TaxID=33169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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1445 DVSERPS 1451
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ORFNames=ABL133C;
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Spacer
                                                                                                                                                                                                                    Pfam; PF05986; ADAM spacer1; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; TSP 1; 13.
SMART; SM00209; TSP1; 15.
                                                     EMBL; AF261918; AAF89106.1; -.
EMBL; AF488803; AAO15765.1; -.
EMBL; AB037733; BAA92550.1; -.
HSSP; P07996; 1LSL.
MEROPS; M12.021; -.
Genew, HGNC:13202; ADAMTS9.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "ADAMTS 9, a novel member of the ADAM-TS/Metallospondin gene family.";
               O9P2N4; O9NR29; Created)
16-OCT-2001 (Rel. 40, Created)
11-0-OCT-2003 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
ADAMTS-9 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 9) (ADAM-TS 9) (ADAM-TS9).
Name-ADAMTS9; Syronyms=KIAA1312;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:65-73(2000).
-I- FUNCTION: Cleaves the large aggregating proteoglycans, aggrecan
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION.
MEDLINE=22513925; PubMed=12514189; DOI=10.1074/jbc.M211009200;
Somerville R.P., Longpre J.-M., Jungers K.A., Engle J.M., Ross M.,
Evanko S., Wight T.N., Leduc R., Apte S.S.;
Evanko S., Wight T.N., Leduc R., Apte S.S.;
subfamily related to Caenorhabditis elegans GON-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms=3;
Name=1; Synonyms=ADAMTS-9B;
Isofd=Q9P2N4-3; Sequence=Displayed;
Name=2; Synonyms=Long:
Isofd=Q9P2N4-1; Sequence=VSP 007548, VSP 007549;
Note=May result from the retention of an intron in the cDNA
                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                          TISSUE=Fetal;
MEDLINE=20396138; PubMed=10936055; DOI=10.1006/geno.2000.6246;
Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A.,
Maki R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the peptidase M12B family. SIMILARITY: Contains 1 disintegrin-like domain. SIMILARITY: Contains 1 GON domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 15 TSP type-1 domains.
          PRT; 1935 AA
                                                                                                                                                                                                                                                                                         SEQUENCE OF 159-1935 FROM N.A. (ISOFORM 2).
                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                           Genomics 67:343-350(2000).
          STANDARD;
                                                                                                               NCBI_TaxID=9606;
         HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01421; Kepurini,
Pfam; PF00090; TSP1; 13.
SWART; SW00209; TSP1; 13.
PROSITE; PS00146; CYSTEINE SWITCH; PALSE NEG.
PROSITE; PS00427; DISINTEGRIN 1; FALSE NEG.
PROSITE; PS00427; DISINTEGRIN 1; FALSE NEG.
PROSITE; PS00142; DISINTEGRIN 2; FALSE NEG.
PROSITE; PS00142; ZINC PROTEASE; 1.
Alternative splicing; Extracellular matrix; Glycoprotein; Hydrolase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.
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Zinc (catalytic) (By simila
                                                                                                                                                                                                                                                                                                    GO; GO:0008237; F:metallopeptidase activity; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0005216; P:glycoprotein catabolism; TAS.
InterPro; IPR010294; ADAM spacer1.
InterPro; IPR011762; Disintegrin.
InterPro; IPR001818; Pept M10A M12B.
InterPro; IPR001819; Pept M10A M12B.
InterPro; IPR001890; Peptidase M12B.
InterPro; IPR001890; Peptidase M12B.
InterPro; IPR0008870; Peptidase M12B.
InterPro; IPR0008870; Peptidase M12B.
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Zinc (catalytic) (
Zinc (catalytic) ()
N-linked (GlCNAc.)
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TSP type-1 1.
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TSP type-1 3
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TSP type-1 5
TSP type-1 6
TSP type-1 7
TSP type-1 9
TSP type-1 1
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SIMILARITY: Contains 1 ferritin-like diiron domain.
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-i- COFACTOR: Binds 1 heme b (iron-protoporphyrin IX) group per monomer (Potential).
-i- SUBUNIT: Oligomer of 24 identical subunits (By similarity).
-i- MISCELLANBROUS: The di-iron binding site functions as active site where iron ions are oxidized from iron(II) to iron(III) before they are stored (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98072426; PubMed=9409768; DOI=10.1016/S0378-1119(97)00424-1;
                                      (in isoform 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Magnetospirillum magnetotacticum (Aquaspirillum magnetotacticum).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Magnetospirillum.
             (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bertani L.E., Huang J.S., Weir B.A., Kirschvink J.L.,
"Evidence for two types of subunits in the bacterioferritin of
Magnetospirillum magnetotacticum.";
Gene 201:31-36(1997).
| 1072 | CLUTCGKH -> VRWEGCYFP (in isofoold | 1072 | CLUTCGKH -> VRWEGCYFP (in isofoold | 1072 | CLUTCGKH -> VRWEGCYFP (in isofoold | 1073 | 1935 | Missing (in isofoold | 1074 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 | 1075 |
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 1; Length 1935;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2004 (Rel. 44, Last annotation update)
Bacterioferritin subunit 1 (BFR 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 AA
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0; Mismatches
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InterPro, IPR009078; Ferritin/RR like.
InterPro, IPR008331; Ferritin Dps.
InterPro, IPR009040; Ferritin like.
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PRINTS; PR00601; BACFERRITIN.
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Best Local Similarity
Matches 6; Conserv
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DR TIGREAMS; TIGR00754; bfr; 1.

DR PROSITE; PS00965; FERRITIN, 1.16.

DR PROSITE; PS00965; FERRITIN LIKE, 1.

KW Heme; Iron; Iron storage; Wetal-binding.

FT DOMAIN 1 147

FT METAL 18 18 Iron 1 (By similarity).

FT METAL 51 51 Iron 1 (By similarity).

FT METAL 54 94 Iron 2 (By similarity).

FT METAL 129 129 Iron 2 (By similarity).

FT METAL 132 Iron 2 (By similarity).
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Search completed: October 14, 2005, 16:19:57 Job time: 48.5938 secs

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Sequence:

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US-09-383-667-14
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4555, Ap
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                                                                                                                                                                     October 14, 2005, 16:00:04; Search time 13.7812 Seconds (without alignments) 37.917 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-652-816A-15
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US-09-484-84-84-12
US-09-484-84-12
US-09-484-12
US-09-526-098-10
US-09-526-098-10
US-09-383-16-10
US-09-383-16-10
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US-09-490-016-785-3
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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Sequence 43922, A Sequence 18161, A Sequence 2750, App Sequence 11, Appl Sequence 11, Appl Sequence 2, Appl Sequence 15, App Sequence 11, Appl Sequence 11, Appl Sequence 17949, A Sequence 32910, App Sequence 38090, A Sequence 23912, App Sequence 4891, App Sequence 23912, App Sequence 4891, App Sequence 23912, App Sequence 23912, App Sequence 23912, App Sequence 23912, App Sequence 3333, App Sequence 23912, App Sequence 3333, App Sequence 23912, App Sequence 3333, A
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Patent No. 5872215

GENERAL INFORMATION:

APPLICANT: OBDOUR., JK

APPLICANT: Allen, DJ

APPLICANT: Allen, DJ

TITLE OF INVENTION: methods.

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Materhall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JUS-09-383-667-14

| Sequence 14. Application US/09383667
| Sequence 14. Application US/09383667
| Patent No. 6624295
| GENERAL INFORMATION:
| APPLICANT: Adams, Camelia W. APPLICANT: Bevoux, Brigitte
| APPLICANT: Bas, Philip E. APPLICANT: Hass, Philip E. APPLICANT: Widlee, J. Kevin | APPLICANT: Kirchnfer, Daniel APPLICANT: Kirchnfer, Daniel APPLICANT: Kirchnfer, Daniel APPLICANT: Kirchnfer, Daniel APPLICANT: Suggett, Shelley TITLE OF INVENTION: Plof R. Settle REFERENCE: Plof 12. CURRENT APPLICATION NUMBER: US 60/098,233 | EARLIER APPLICATION NUMBER: US 60/122,767 | LENGTH: 7 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 7;
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US-09-538-09-423
US-09-321-987B-2
US-09-321-987B-2
US-09-074-658-15
US-09-074-658-11
US-09-107-532A-7296
US-09-278-796A-17949
US-09-270-767-38080
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ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 166 K Street, N.W., Suite 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: Z7,794
RECISTRATION NUMBER: Z7,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELEFORMUNICATION 110FORMATION:
TELEFORMUNICATION 10FORMATION:
TELEFORMUNICATION 10FORMATION:
TELEFORMUNICATION 10FORMATION:
TELEFORMUNICATION 10FORMATION:
INPORMATION POR SEQ 1D NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
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APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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COUNTRY: USA
ZIP: 20006
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Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: RABDIM, Achim
APPLICANT: Pack, Peter
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Plucekthum, Andreas
APPLICANT: Plucekthum, Andreas
APPLICANT: OF INVENTION: Protein/(Poly)peptide libraries
ITILE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 35; DB 2; Length 111; 100.0%; Pred. No. 1.9; ive 0; Mismatches 0; Indel8
                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
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APPLICATION NUMBER:
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BRIOR APPLICATION NUMBER:
BRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
BRIOR APPLICATION NUMBER:
B
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312-474-6300 INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 111 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 DVSKRPS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVSKRPS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
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Gaps

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Indels

Gaps

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Gaps
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COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBW PC compatible
COMPUTER: IBW PC compatible
COMPUTER: IBW PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-FEB-1995
FILING DATE: 18-AUG-1995
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ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITR: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 35; DB 4; Length 112; 100.0%; Pred. No. 1.9; ive 0; Mismatches 0; Indels
                                        Length 112;
                                                                                  IndelB
                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
Pack, Peter
Ilag, vic
Ge, Liming
Moroney, Simon
Pluckthum, Andreas
TILE OF INVENTION: Protein/(Poly) peptide libraries
                                          100.0%; Score 35; DB 4
                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-490-324-19
                                                                                                                                                                                                                                                                Sequence 19, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 25, Application US/09383667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 112 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
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                                          Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                          1 DVSKRPS 7
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US-09-383-667-25
      US-09-490-153-19
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US-09-490-324-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09490153

Patent No. 6706484

GENERAL INFORMATION:

APPLICANT: Kaappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                               DB 4; Length 112;
                                                                                                                                                                                                                                                                                                                                                                     0; Indels
RAME: Colin G. Sandercock, Esq.
REGISTATION UNDERF: 31.298
REFERENCE/DCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERESTICS:
LENGTH: 112 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             100.0%; Score 35; DB 4 100.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                            STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-490-070A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212)596-9000
TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID No: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 112 amino acids
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
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LEWIS, ALAN PETER VENTION: PRODUCTION OF ANTIBODIES

ERNST & KURZ

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TITLE OF INVENTION: PRODUCTII
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG,
STREET: 555 THIRTEENTH ST.
                                                                                          STREET: 555 THIR CITY: WASHINGTON
                                                                                                                                 STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local &
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Fatent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchcold, Peter
APPLICANT: Berchcold, Peter
APPLICANT: Berchcold, Peter
TITLE OF INVENTION: ANT-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 10054-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT APPLICATION NUMBER: US/09/424,840B
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
SPRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFULD NO 125
SEQ ID NO 125
GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Adams, Camelia W.
APPLICANT: Beron, Dan L.
APPLICANT: Beron, Dan L.
APPLICANT: Base, Philip E.
APPLICANT: Hass, Philip E.
APPLICANT: Kirchofer, Joniel
APPLICANT: Kirchofer, Daniel
APPLICANT: Sugget, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2
CURRENT APPLICATION NUMBER: US 60/98,233
FARLIER APPLICATION NUMBER: US 60/98,233
EARLIER APPLICATION NUMBER: US 60/98,233
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER PILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 4; Length 7; Pred. No. 4.1e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.6%; Score 31; DB 4; Length 7;
85.7%; Pred. No. 4.1e+05;
ive 1; Mismatches 0; Indels
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-09-383-667-25
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                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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Sequence 10, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS;
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                           OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 2;
Pred. No. 33;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
CIIY: Alexandria
                                                                                                                                 APPLICATION:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/ACENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REGISTRATION NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 783-6040
TELEFAX: (202) 783-6040
TELEFAX: (202) 783-603:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 235 amino acids
amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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nes 6; Conserv
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US-08-378-939-12; Sequence 12, Application US/08378939; Sequence 12, Sequence 12, EST6961; Patent No. 2876961; GENERAL INFORMATION: APPLICANT: CROWE, JAMES SCOTT

RESULT 9

Gaps

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Indels

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Mismatches

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5; Conservative
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US-09-949-016-7859
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Matches
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMANCEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Absandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                      Gapa
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                                                                                                                                                                                                                                                                               Score 31; DB 3; Length 236;
Pred. No. 33;
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: 09/383,916
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                             35,030
FR: 012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09526098 Patent No. 6492134 GENERAL INFORMATION:
             NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPRX: 703-836-2021
                                                                                                   TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.6%;
71.4%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4
Ellocal Similarity 71.4
Si Conservative
                                                                                                                                                                                 ; TYPE: amino acid
; TOPOLOGY: linear
; MOLEGULE TYPE: protein
US-08-487-550-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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71 DINKRPS 77
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                        1 DVSKRPS 7
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ZIP: 22314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-526-098-10
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7859, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL00130, 1009, 1009, 1006
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 012/12-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                   US-09-383-916-10
; Sequence 10, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
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71.4%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
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71 DINKRPS 77
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71 DINKRPS 77
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Sequence 13, Application US/09369364A

Sequence 13, Application US/09369364A

Sequence 13, Application US/09369364A

GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/40/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A

CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1882
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; Patent No. 6300064
; GENERAL INFORMATION:
APPLICANT: Raappik, Achim
APPLICANT: Pack, Peter
CAPLICANT: Pack, Peter
APPLICANT: Pack, Peter
APPLICANT: Occoper, Simon
APPLICANT: Pocchey, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
WUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens ADAMTS-9
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LOCATION: (468)
OTHER INFORMATION: Xaa = C
NAME/KEY: MOD RES
LOCATION: (521)
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OTHER INFORMATION: Xaa = Y
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                 ORGANISM: Human
                                                                                                                                                                                                                                                         US-09-949-016-7859
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US-09-369-364A-13
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Gaps
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                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-A0G-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Halley, Jr., ESQ.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
MEDIUM TO NOT NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 3; Length 110;
Pred. No. 25;
0; Mismatches 1; Indels
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
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Best Local Similarity 85.79
Elector 6; Conservative
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MOLECULE TYPE: protein
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                      CITY: New York STATE: New York
                                                                             USA
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                                                                             COUNTRY:
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Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

US-10-293-418-1927
US-110-293-418-1927
US-110-291-692-33
US-10-981-692-33
US-10-981-692-36
US-10-293-418-1926
US-10-293-418-1926
US-10-293-418-1926
US-10-293-418-1913
US-10-293-418-1913
US-10-293-418-1913
US-10-293-418-1913
US-10-293-418-1928
US-10-293-418-1938

Sequence

Sequence Seq

Sequence Sequence S

Sequence Sequence Sequence

ALIGNMENTS

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Sequence 98, Appl
Sequence 1, Appl
Sequence 61, Appl
Sequence 12, Appl
Sequence 1898, Ap
Sequence 2055, Ap
Sequence 2055, Ap
Sequence 24, Appl
Sequence 24, Appl
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                                                                                                                                                                            October 14, 2005, 16:20:10 ; Search time 49.7656 Seconds (without alignments) 58.615 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Contact | Cont
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-10-453-669-98
US-10-360-828-61
US-10-360-828-61
US-10-916-758-42
US-09-880-748-1898
US-10-293-418-1898
US-10-293-418-2055
US-10-291-692-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1859788 segs, 416717961 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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35
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Match
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Perfect score:
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Maximum DB
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Sequence 98, Application US/10308817
Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SEQ ID NO 98
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-453-698-98
; Sequence 98, Application US/10453698
; Publication No. US20040038308A1
; Publication No. WS20040038308A1
; APPLICANT: Rother, Russell
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DVSKRPS 58
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                  , ORGANISM: human
US-10-308-817-98
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Query Match
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Sequence 61, Application US/10360828

Publication No. US20310206909A1

Sequence 61, Application US/10360828

Publication No. US20310206909A1

APPLICANT: Hua, Shaobing

APPLICANT: Hua, Shaobing

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS

FILE REFERRING: 2563-727

CURRENT APPLICATION NUMBER: US/10/360,828

CURRENT FILING DATE: 2003-02-07

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-04-25

NUMBER OF SEQ ID NOS: 64
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                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 15; Length 99; 100.0%; Pred. No. 15; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-14. Application US/10447331

Publication No. US20030219434A1

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Carter, Paul J.

APPLICANT: Carter, Paul J.

TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND TITLE OF INVENTION: DIAGNOSIS

FILE REFERENCE: GENERY.122A

CURRENT APPLICATION NUMBER: US/10/447,331

CURRENT FILING DATE: 2003-05-29

PRIOR PILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 110
TITLE OF INVENTION: HYBRID ANTIBODIES FILE REFERENCE: 82 CIP (1087-37 CIP) CURRENT APPLICATION NUMBER: US/10/453,698 CURRENT FILING DATE: 2003-06-03 NUMBER OF SEQ ID NOS: 196 SOFTWARE: Patentin version 3.2 SEQ ID NO 98 LENGTH: 99
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 7; Conservative
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US-10-447-331-1
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ORGANISM: human
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US-10-447-331-1
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben tal.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PPS-21
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT PILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; RIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR PILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; RIOR APPLICATION NUMBER: 60/293,499
; RIOR APPLICATION NUMBER: 60/293,499
; RIOR PILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 3239
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US-10-916-758-42
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100.0%; Pred. No. 18;
tive 0; Mismatches 0;
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100.0%; Pred. No. 17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 42, Application US/10916758
; Sequence 42, Application US/10916758
; Publication No. US20050180977A1
; GENERAL INFORMATION:
; APPLICANT: Madison, Edwin L.
; TITLE OF INVENTION: ENDOTHELIASE-2 LIGANDS
; FILE REFERENCE: 10280-065001
; CURRENT APPLICATION NUMBER: US/10/916,758
; CURRENT PILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/520,164
; PRIOR APPLICATION NUMBER: US 60/520,164
; PRIOR FILING DATE: 2003-10-14
; PRIOR FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 113
; SEQ ID NO 42
: LENGTH: 118
                                                                                                                            ; FEATURE:
; OTHER INFORMATION: VL of scFv Ab124
US-10-360-828-61
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ORGANISM: Artificial Sequence
SOFTWARE: Patentin version 3.1
SEQ ID NO 61
LENGTH: 111
                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 7; Conservative
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52 DVSKRPS 58
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Best Local Similarity
Matches 7; Conserv
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US-09-880-748-1898
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Sequence 24, Application US/10981692
Publication No. US20050163777A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
FILE REFERENCE: PF590P1
CURRENT APPLICATION NUMBER: US/10/981,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2055, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVERTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: 08/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR PRIOR APPLICATION NUMBER: 60/210,210

PRIOR APPLICATION NUMBER: 60/210,210

PRIOR PRIOR APPLICATION NUMBER: 60/210,210

PRIOR PRIOR PRILING DATE: 2001-01-17

PRIOR PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

FEATURE FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247
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PRIOR FILING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2055
LENGTH: 241
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-880-748-2055
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US-10-293-418-2055
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US-10-981-692-24
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JAPPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT APPLICATION NUMBER: US/31,469
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR PILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/39,499
PRIOR PILING DATE: 2001-66-15

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15

PRIOR PPLICATION NUMBER: 60/273,379
PRIOR PPLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2000-06-17

PRIOR PLING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247
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; Sequence 2055, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFREENCE: PF5.23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR PELICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1898
LENGTH: 240
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                         ; ORGANISM: Homo sapiens
US-09-880-748-1898
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US-10-293-418-1898
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Best Local Similarity
Matches 7; Conserv
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US-10-293-418-1927
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| Sequence 40, Application to US/20050163777A1
| Sequence 40, Application to US/20050163777A1
| GENERAL INFORMATION:
| APPLICAMT: Rosen et al. |
| TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PF590P1
| CURRENT APPLICATION NUMBER: US/10/981,692
| CURRENT PELICATION NUMBER: US/10/981,692
| PRIOR PELICATION NUMBER: PCT/US03/16802
| PRIOR PELICATION NUMBER: 60/383,802
| PRIOR PELICATION NUMBER: 60/383,802
| NUMBER OF SEQ ID NOS: 76
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 40
| LENGTH: 242
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS;
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS;
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
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Best Local Similarity 100.0%; Score 35; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR FILING DATE: 2003-05-29
PRIOR PELLING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
LENGTH: 242
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US-10-981-692-40
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Best Local Similarity 100.0
Matches 7; Conservative
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US-10-981-692-40
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Sequence 29, Application US/10981692;
Publication No. US2005016377A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PF590P1
CURRENT APPLICATION NUMBER: US/10/981,692
CURRENT FILING DATE: 2004-11-05
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FILE REFERENCE: PF523P2
CURRENT ANDION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/31,469
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/240,817
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-16
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FLING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SERQIA DO 0.1927
LENGTH: 243
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; Publication No. US20030223996A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100..
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Best Local Similarity 100.
Matches 7; Conservative
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US-10-293-418-1927
                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1927
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Publication No. US20050163777A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

TITLE OF INVENTION: MADER: US/10/981,692

CURRENT APPLICATION NUMBER: US/10/981,692

FRICR APPLICATION NUMBER: PG7/US03/16802

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-30

PRIOR FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.1

SEQ ID NO 33

LENGTH: 243

TYPE: PRT

PRATURE: PRT

REAUTINE: REAUTION OF ARTHURE: REAUTION OF SEQUENCE

SOFTWARE: PRT

CONCANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 35; DB 18; Length 243; 100.0%; Pred. No. 37; tive 0; Mismatches 0; Indels (
PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: 60/383,802
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
ERO ID NO 29
LENGTH: 243
                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: N024E07 scFv
US-10-981-692-29
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; OTHER INFORMATION: N023E01 sCFV
US-10-981-692-33
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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US-10-981-692-33
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Search completed: October 14, 2005, 17:00:44 Job time : 50.7656 secs

183 DVSKRPS 189

1 DVSKRPS 7

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                Copyright
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- protein search, using sw model OM protein October 14, 2005, 15:51:19 ; Search time 84.5625 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-15 58

1 AAWDDSLSEFL 11 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database

geneeqp1980s: *
geneeqp1990s: *
geneeqp2000s: *
geneeqp2001s: *
geneeqp2001s: *
geneeqp2003s: *
geneeqp2003bs: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length DB	08	ΙD	Description
1	58	100.0	11	1 6	AAY79073	Aay79073 Anti-fact
7	58	100.0	104	~	AAR80087	
e	58	100.0	7	7	AAW95485	
4	28	100.0		4	AAU02544	
ស	58	100.0		4	AAU02558	Aau02558 Anti-adip
9	58	100.0		4	AAU02612	Aau02612 Anti-adip
7	58	100.0	110	4	AAU02627	Aau02627 Anti-adip
æ	58	100.0	110	4	AAU02629	Aau02629 Anti-adir
σ	58	100.0		~	AAW19883	Aaw19883 CEA-speci
10	58	100.0	111	4	AAU02542	Aau02542 Anti-adip
11	58	100.0	111	4	AAU02551	Aau02551 Anti-adip
15	58	100.0		4	AAU02585	
13	58	100.0	111	4	AAU02606	Aau02606 Anti-adir
14	58	100.0	242	œ	ADG34301	Adg34301 Neurokini
15	58	100.0		œ	ADG34317	Adg34317 Neurokini
16	58	100.0		ß	ABP45916	Abp45916 Human BLy
17	58	100.0	243	7	ADG96743	Adg96743 Single ch
18	28	100.0	243	8	ADG34310	
19	58	100.0	243	8	ADG34306	Adg34306 Neurokin:
70	58	100.0	244	80	ADG34303	Adg34303 Neurokini
21	58	100.0	245	ß	ABP45915	
22	58	100.0		7	ADG96742	Adg96742 Single ch
23	28	100.0	245	7	ADG98057	Adg98057 TNF proli
24	58	100.0	245	8	ADE83862	Chen
25	58	100.0	245	œ	ADG34308	Adg34308 Neurokini

246 5 ABP45902 246 7 ADG96733 246 7 ADG96739 246 8 ADG96729 247 5 ABP45871 247 5 ABP45823 247 5 ABP45823 247 7 ADG30413 247 7 ADG30413 247 7 ADG3042 247 7 ADG30649 247 7 ADG96750	Abp45902 Human BLy Abp45906 Human BLy Adg96733 Single ch	9242	Human Human Human	Human Human Single	
	ABP45902 ABP45906 ADG96733	ADG96729 ADE83872 ABP45671 ABP45432	ABP45923 ABP45917 ABP45696	Abg30413 Abg30413 Abg96715 Abg96715 Abg96498	ADG96744 ADG96259 ADG96750 ADG96523 ADE83874
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5.88	22 23 24	3 3 3 8 3 3 3 8	ლ ლ ლ ი ლ 4- დ ი	1 U U U 4 5 L B O O	4 4 4 4 4 4 4 6 4 6

ALIGNMENTS

Complementarity determining region 3; CDR3; antibody; Gla domain; factor IX/IXis, blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. Anti-factor IX/IXa antibody L chain V domain CDR3 amino acid sequence. AAY79073 standard; peptide; 11 AA (first entry) 12-JUN-2000 AAY79073; AAY79073

Homo sapiens.

WO200012562-A1.

09-MAR-2000

99WO-US019453. 26-AUG-1999;

98US-0098233P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC

Kirchhofer D; Hass PE, Judice JK, Adams CW, Devaux B, Eaton DL, Suggett S;

WPI; 2000-256595/22.

こ せん そうけいりょうりゅうりょう とりょう とんりょく アス

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 3 (CDR3) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXA is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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RESULT 3
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cells and platelets. Compositions comprising the antibodies are used for the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (FICA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           generating a
in phage
                                                                                                                                                                               Gaps
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Titmas RC, Williams RO;
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/note= "complimentarity determining region 1"
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:e= "complementarity dtermining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Production of catalytic antibodies displayed on phage - by gene library of antibody-derived domains and expressing it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining region
                                                                                                                                                      Length 11;
                                                                                                                                                      100.0%; Score 58; DB 3; Length 11
100.0%; Pred. No. 0.0022;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         Human derived light chain RT3 phage antibody.
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94. .104
/note= "framework region 4"
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/note= "framework region 1"
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:e= "framework region 2"
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.e= "complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                      AAR80087 standard; protein; 104 AA.
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                                                                                                                                                                                                                                                                                                                                   (first entry)
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Martin MT,
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                                                                                                                                                                                                      1 AAWDDSLSEFL
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N-PSDB; AAT04634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IGEN-) IGEN INC.
                                                                                                                                Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                   23-MAY-1996
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Kenten JH,
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Disclosure, Fig 20; 133pp, English.

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comprises generating a gene library of antibody-derived domains inserting
coding into a phage expression vector and isolating the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The catalytic antibodies can be isolated by preparing an antigen; optionally immunising an animal with the antigen; generating a library of VH and VL domains from the immunised animal; cloning the VH and VL domains into a phage expression vector to generate phage display
                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catalytic; antibody; phage display; immunising; phage expression vector;
     phage antibody.
AAT04634 encodes AAR80087 human derived light chain RT3 phage antibody. The DNA was used in the prepn. of catalytic antibody (CA) producing bacteriophage. The CAs can be used to activate/deactivate a biological function in an animal by enhancing the rate of cleavage, or formation a specific bond within a mol. in vivo
                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     Human-derived RT3 phage antibody light chain genetic sequence.
                                                                                                                               100.0%; Score 58; DB 2; Length 104; 100.0%; Pred. No. 0.023; ive 0; Mismatches 0; Indels
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Mccafferty J, Titmas RC;
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                                                                                                                                                                                                                                                                                                                      AAW95485 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00273146.
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Kenten JH, Chiswell D, Mc
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                    1 AAWDDSLSEFL 11
                                                                                                                                                                                                                                 83 AAWDDSLSEFL 93
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DARSLEY M J.
TITMAS R C.
MARTIN M T.
KENTEN J H.
SMITH R.
FITZGERALD K.
WILLIAMS R O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCCAFFERTY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-105036/09.
                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prodrug; scFV; RT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX00884.
                                                                                                   Sequence 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding into
antibodies
                                                                                                                                                                                                                                                                                                                                                     AAW95485;
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(CHIS/)
(DARS/)
(TITM/)
(MART/)
(KENT/)
(SMIT/)
(FITZ/)
                                                                                                                                                                     Matches
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abdominal fat associated with heart disease

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ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obserty and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
chectable labels such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies, where the phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic sequences which can be used for in vivo activation of a producy. Sequences AAW95484-489 represent genetic sequences of heavy and light chains of RT3 specific phage antibodies selected from a naive human phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody, adipocyte, heavy chain, light chain, obesity, fat, heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 2; Length 104;
Pred. No. 0.023;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-adipocyte monoclonal antibody light chain, FAT 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                               antibody library
                                                                                                                                                                                                                                                                                                                                                                      Sequence 104 AA;
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain. light chain,
and heavy chain complementarity determining regions (CDR) of the
cinvention. The antibodies can be used in the treatment of obesity and
cinvention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
considered the mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
cused in methods of diagnosis in human subjects e.g. to determine the
considered antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
considered than undergoing surgery to remove excess fat. Antibodies
considered with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                            Score 58; DB 4; Length 109;
Pred. No. 0.024;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Antibody, adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                              Anti-adipocyte monoclonal antibody light chain, FAT 44.
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                                                                                                                                                                                                                                     AAU02558 standard; protein; 110 AA.
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                                  100.0%;
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                                             Local Similarity 100 nes 11; Conservative
                                                                                                                                           90 AAWDDSLSEFL 100
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                                                                                                         1 AAWDDSLSEFL
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Sequence 109 AA;
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                                  Query Match
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AMU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte and interporte and interporte to detect or determine the presence or level of adipocytes in a call or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; adipocyte; heavy chain; light chain; obesity; fat;
                                                                                                                                                        Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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                                                                                                            Anti-adipocyte monoclonal antibody light chain, FAT 112.
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                                                                   (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 110 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese for different types of fat deposits can alternative means of treatment for obese for different types of fat deposits can alternative means of intra-abdominal fat associated with heart disease
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                                                                                                                                                                                                                                                                                                    Anti-adipocyte monoclonal antibody light chain, FAT 99.
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                                                                                                                                                          AAU02612 standard; protein; 110 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0158812P.
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90 AAWDDSLSEFL 100
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AAWDDSLSEFL 11
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AAU02627 ID AAU0 RESULT 7

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29-AUG-2001 (first entry)
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Matches 11; Conservative
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                                                                                    WO9720932-A1.
                                                                                                                                    09-DEC-1996;
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sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-trugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
of complement mediated lysis. The antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
of complement mediated lysis. The antibodies binding specifically to
adipocyte antigon on the surface of an adipocyte to determine the
presence of adipocyte antigon on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                                                                                                                                                                     Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.
                                                                                                                                                (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
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                                                                                                                                                                         Vaughan TJ;
                                                                                                                                                                                                                                                                                      Claim 1; Page 173; 182pp; English
                                                                                                                       99US-0158812P.
                                                                                               11-OCT-2000; 2000WO-GB003900.
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                        Homo sapiens
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This polypeptide sequence comprises the light chain variable region (VL) of human carcinoembryonic antigen (hCEA)-specific antibodies CEA1, CEA2 and CEA3. VH (AAT7213-35) gene sequences were obtained for anti-hCEA antibodies CEA1-CEBA7 (see AAW19876-85). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10-8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-83 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7, or their CEN sequences, as well as CEA6 VH and VL variants (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer.
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/label= CDR3
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain. light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cinvention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
can be used as a therapeutic itself. Antibodies binding specifically to
cappement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
cused in methods of diagnosis in human subjects e.g. to determine the
cused in methods can antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
cor different types of fat deposite can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                    Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                                                                        Claim 1; Page 124; 182pp; English.
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hes 11; Conservative
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                    2001-282031/29
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                    WPI; 2001-282031
N-PSDB; AAS03451
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intraabdominal fat associated with heart disease
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                                                                                                                (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 118-119; 182pp; English.
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N-PSDB; AAS03442.
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Query Match Matches 29-AUG-2001

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                      AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
convertion. The antibodies can be used in the treatment of obesity and
convertion of the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
can be used as a therapeutic itself. Antibodies binding specifically to
cappenent mediated lysis. The antibodies binding specifically to
cappenent mediated lysis. The antibodies binding specifically to
detectable label such as radiolabel, fluorescent or chemical group and
cappenent antibodies antibodies in human subjects e.g. to determine the
cappenent antibodies on the surface of an adipocyte of determine the
cappenent antibodies an alternative means of treatment for obese
cappenent than undergoing surgery to remove excess fat. Antibodies
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abdominal fat associated with heart disease
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Claim 1; Page 146; 182pp; English.
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Best Local Similarity 100.
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N-PSDB; AAS03506.
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can be used as a therapeutic itself. Antibodies binding specifically to adjocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adjocyte antigen on the surface of an adjocyte to detect or determine the presence or level of adjocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese fatient types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 58; DB 4; Length 111; 100.0%; Pred. No. 0.025; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 24; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG34301 standard; protein; 242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurokinin B antibody SEQ ID NO:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-2003; 2003WO-US016802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2002; 2002US-0383802P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 AAWDDSLSEFL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAWDDSLSEFL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2004-053456/05.
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Best Local Similarity
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nes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 111 AA;
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221 AAWDDSLSEFL 231

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                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                         antibody; neurokinin B; hypotensive; gynaecological; gene therapy; hypertension; pre-eclampsia; NKB.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 58; DB 8; Length 242; 100.0%; Pred. No. 0.056; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 40; 127pp; English.
                            ADG34317 standard; protein; 242 AA.
                                                                                                                Neurokinin B antibody SEQ ID NO:40.
                                                                                                                                                                                                                                                                        29-MAY-2003; 2003WO-US016802.
                                                                                                                                                                                                                                                                                                   30-MAY-2002; 2002US-0383802P.
                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                    (first entry)
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAWDDSLSEFL 11
                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Ruben SM;
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N-PSDB; ADG34298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 242 AA;
                                                                                                                                                                                                                WO2003102136-A2.
                                                                                    26-FEB-2004
                                                                                                                                                                                                                                            11-DEC-2003.
                                                                                                                                                                                    Synthetic.
                                                        ADG34317;
RESULT 15
                ADG34317
                                          ð
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Search completed: October 14, 2005, 16:12:42 Job time : 84.5625 secs

221 AAWDDSLSEFL 231

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 14, 2005, 16:02:59; Search time 15.2969 Seconds (without alignments) 69.190 Million cell updates/sec

US-10-614-959-15 58 Title: Perfect score:

1 AAWDDSLSEFL 11 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	43	74.1	96	5	S36048	Iq lambda chain -
7	43	74.1	129	~	S78058	lambda
٣	43	74.1	235	~	S25750	ampda
4	41	70.7	112	Н	LIHUMM	
S	40	69.0	95	~	S49571	lambda
9	40	69.0	98	7	S36047	lambda
7	40	69.0	98	~	S36046	lambda
80	40	69.0	109	-	LIHUWA	
6	40	69.0	117	~	S23627	lambda
10	40	0.69	149	7	S23626	lambda
11	40	69.0	233	~	S25752	Ig lambda chain -
12	40	69.0	234	~	S25757	
13	40	69.0	235	~	S25754	Ig lambda chain -
14	40	69.0	355	~	E87394	
15	40	69.0	497	~	G95983	probable glycerol
16	40	69.0	502	~	S49113	cal
17	40		4367	-	B54802	
18	39	67.2	110	~	S57428	Ig light chain V-J
19	39		112	~	D44151	מו
20	39		130	7	S78057	
21	39		397	-	OKBOB2	protein kinase (EC
22	39		1995	~	T08166	probable membrane
23	39		4344	н	A53489	dynein heavy chain
24	38	65.5	210	~	G84751	hypothetical prote
25	38	ď.	329	~	T18622	
56	38	•	423	~	S41289	cal
27	38	S.	443	~	T30619	probable serine/th
28	38	S.	842	~	B55853	outer membrane ush
53	38	•	882	7	WMBY3L	ribonucleoside-dip

hypothetical prote	conserved hypothet	outer membrane pro	conserved hypothet	thiamin biosynthes	probable thiamin b	probable PPE prote	hypothetical prote	CFTR protein - Afr	interferon alpha-I	interferon alpha-I	interferon alpha-I	interferon alpha-I	insertion element	probable sugar tra	hypothetical prote
C83366	T40104	AH0147	T40102	H84228	F84698	A70931	B69798	S23756	IVHOA1	IVHOA2	IVHOA3	IVHOA4	F81855	C98208	AF3078
7	7	~	~	0	Ŋ	N	N	0	-4	н	н	н	N	N	~
166	259	371	395	476	644	655	857	1485	184	184	184	184	227	280	280
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64.7	63	63.8	63	63	63	63	63.8	63	62	62	62	62	62	62.1	62
37.5	37	37	37	37	37	37	37	37	36	36	36	36	36	36	36
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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1g Jambda chain - human (fragment)
Ig Jambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36048; S36049
E:Williams, S.C.
                                                                                                                                                                  Bubmitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36048
A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-98 <WIL>
```

A;Cross-references: EMBL:Z22189; NID:g312294; PIDN:CAA80199.1; PID:g312295; EMBL:Z22190 (S.Guperfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin pomology F;15-91/Domain: immunoglobulin homology <IMM>

ö Length 98; 0; Indels 74.1%; Score 43; DB 2; 100.0%; Pred. No. 1.3; ative 0; Mismatches Query Match
Best Local Similarity 100.
Matches 8; Conservative

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Gaps

90 AAWDDSLS 97 œ 1 AAWDDSLS ò 셤

RESULT 2 S78058

Ig lambda chain precursor V-J region (clone mAB 67VL) - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C;Accession: S78058; S23723 R;Harindranath, N. submitted to the EMBL Data Library, August 1990 A;Reference number: S78051

A;Molecule type: mRNA
A;Residues: 1-129 LHAR>
A;Residues: 1-129 LHARS: 1-1

patient. A;Reference number: S23716; MUID:92031262; PMID:1718404 A;Accession: S23723

A,MOLECULE type: mRNA
A,Residues: 19-129 «HAW»
A,Crose-references: EMBL:X54446
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: immunoglobulin
F;1-18/Domain: signal sequence (fragment) #status predicted <SIG>

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Ig lambda chain precursor V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: OS-Mar-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: 849571
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.
R;Giachino, C.; Padovan, B.; Lanzavecchia, A.
R;Giachino, C.; Lanzavecchia, A.
R;Giachin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S;6046
R;Williams, S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36047
R;Williams, S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-95 <GIA>
A;Cross-references: EMBL:Z46625; NID:g575259; PIDN:CAA86595.1; PID:g575260
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Pred. No. 4.4;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.2;
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A;Reference number: 836046
A;Accession: 836046
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A;Reference number: 836046
A;Accession: 836047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
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    AAWDDSLDGYV 101
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76 AAWDDSLT 83
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Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-98 <WIL>
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A; Residues: 1-98 <WIL>
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C; Decises: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C; Accession: $25750
C; Accession: $25750
Eur. J. Immunol. 21 1513-1522, 1991
A; Title: V(Iambda) and J(lambda) —C(lambda) gene segments of the human immunoglobulin lam A; Reference number: $16439; MUID:91257162; PMID:1904362
A; Accession: $25750
A; Accession: $25750
A; Accession: $25750
A; Accession: $25750
C; Cross-references: EMBL: X57815; NID:933729; PIDN:CAA40952.1; PID:933730
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Weywords: heterotetramer; immunoglobulin homology <IMM>
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F;19-129/Froduct: Ig lambda chain (fragment) #status predicted <MAT>F;33-109/Domain: immunoglobulin homology <IMM>
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Pred. No. 3.4;
2; Mismatches 2; Indels
                                                                                                                             Length 129
                                                                                                                                                                                                             Indels
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                                                                                                                         DB 2;
1.7;
                                                                                                74.1%; Sco...
100.0%; Pred. No. 1...
0; Mismatches
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                                                                                       Query Match
Best Local Similarity 100.0
Thea 8; Conservative
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Best Local Similarity 63.6'
Matches 7; Conservative
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C;Accession: S25752
R;Combriato, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
Sur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A; Peference number: S16439; WUID:91257162; PMID:1904362
A;Accession: S25752
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 325;57;
R;Combriato, G:; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lam A;Reference number: S16439; MUID:91257162; PMID:1904362
                                                                                                                                                                                                                                                                                                  Riolee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 811-842, 1992
J. Exp. Med. 175, 811-842, 1992
J. Fitle: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the A; Reference number: $23623; MUID:92156804; PMID:1740665
A; Accession: $23626
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23626
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X59706; NID:g34204; PIDN:CAA42227.1; PID:g34205 (S.Guperfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-110/Domain: immunoglobulin homology <IMM>
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87.5%; Pred. No. 11;
ive 1; Mismatches
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Pred. No. 6.9;
1; Mismatches
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                                                                                                                                                                                      Ig lambda chain V region - human (fragment)
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||||||||:
109 AAWDDSLN 116
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          Influence chain V-I region (Wah) - human

C;Species: Homo sapiens (man)

R;Takahashi, Y.; Takahashi, N.; Tetaert, D.; Putnam, F.W.

A;Accession: A01967; MUID:83221661; PMID:6407018

A;Reference number: A01967; MUID:83221661; PMID:6407018

A;Residues: 1-109 capk.

A;Residues: 4 capk.

A;Residues: 6 capk.

A;Residues: 1-109 capk.

A;Residues: 6 capk.

A;Residues: 1-109 capk.

A;Residues: 6 
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$23627

Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: $23627
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the A;Restdues: preliminary
A;Residues: preliminary
A;Residues: 1-117 < OLE>
A;Status: preliminary
A;Residues: 1-117 < OLE>
A;Cross-references: EMBL:XS9707; NID:g34426; PIDN:CAA42228.1; PID:g34427
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology < IMM>
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                                                                 DB 2; Length 98;
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                                                                                                                           0; Indels
                                                             Score 40; DB 2
Pred. No. 4.4;
1; Mismatches
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Pred. No.
   C; Keywords: heterotetramer; immunoglobulin
                                                                 69.0%;
87.5%;
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Best Local Similarity 87.5'
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Best Local Similarity 80.v.
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1 AAWDDSLS 8

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Job time : 16.2969 secs
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les 7; Conserv
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R; Combriato, G:; Klobeck, H.G.
Ex. J. Timmunol. 21, 131-1522, 1991
A; Title: V(lambda) and J(lambda) c(lambda) gene segments of the human immunoglobulin lam A; Reference number: $16439; MUID: 91257162; PMID: 1904362
A; Accession: $25754
A; Accession: $25754
A; Accession: $25754
A; Seatus: preliminary; translation not shown
A; Molecule type: manA
A; Residues: 1-235 < COM>A; Residues: 1-235 < COM>COM>C; Repertants: Inmunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 150-218/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conserved hypothetical protein CC1169 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: E87394
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
N.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Accession: E87394
A;Status: preliminary
A;Accession: DNA
A;Bosianary
A;Bosianary
A;Bosianary
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C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Homo sapiens (man)
Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                    A;Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;149-217/Domain: immunoglobulin homology <IMM>
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                                                                                                                                             Length 234;
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Pred. No. 11;
1; Mismatches 0; Indels
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Pred. No. 18;
1; Mismatches
                                                                                                                                               Score 40; DB 2
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      lambda chain - human (fragment)
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Similarity 87.5%;
7; Conservative
                                                                                                                                          Query Match 69.0%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                               108 AAWDDSLN 115
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138 SAWDDSLS 145
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Best Local Similarity
Matches 7; Conserv
A;Residues: 1-234 <COM>
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S25754
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RESULT 15

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probable glycerol kinase (EC 2.7.1.30) [imported] - Sinorhizobium meliloti (strain 1021) C;Species: Sinorhizobium meliloti (C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
                                                                                                           Cjaccession: G95983

R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A; Title: The complete sequence of the 1,683-Kb pSymB megaplasmid from the N2-fixing endc A; Reference number: A95842; MUID:21396508; PMID:11481431

A; Accession: G95983

A; Status: preliminary

A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-497 «KUR»
A; Residues: 1-497 «KUR»
A; Cross-references: UNIPROT: O86033; GB: AL591985; PIDN: CAC49535.1; PID: G15141022; GSPDB: C
A; Experimental source: strain 1021, megaplasmid pSymB
A; Raibbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Di.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Reference number: A96039; MUD: 21368234; PMID: 11474104
A; Concents: annotation
C; Genetics:
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Pred. No. 26;
1; Mismatches
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C, Keywords: phosphotransferase
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

October 14, 2005, 15:51:44; Search time 73.2188 Seconds (without alignments) 76.932 Million cell updates/sec Run on:

US-10-614-959-15 58 Title: Perfect score:

1 AAWDDSLSEFL 11 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q96sb0 homo sapien	homo	kluyv	homo	homo	homo	caulc	Q9jk15 rattus norv	Q9npf8 homo sapien	mus ก	O86033 rhizobium m	Q48904 microcystis	Q09475 caenorhabdi		Q87gv3 vibrio para		P24256 bos taurus	Q7z3ml homo sapien	Q8w0b5 oryza sativ	٠.	Q74b13 geobacter s			-			Q67np3 symbiobacte	_	_		Q815w5 bacillus ce
ID	Q96SB0		Q6CLT9			LV1F HUMAN	Q9A9 <u>2</u> 5	CEA2_RAT	CEA2_HUMAN	CEA2_MOUSE	GLPK RHIME	Q489 <u>0</u> 4	YP93 CAEEL	DYHC_NEUCR	Q87G <u>V</u> 3	Q6GMV7	KAPI BOVIN	Q7Z3M1	Q8W0B5	Q6C0Z1	Q74B13	Q7RY83	Q98TR8	YCX7_CHLRE	DYHC_EMENI	Q73YE0	Q67NP3	Q31358	Q631V6	Q72Y69	Q815W5
% Query Match Length DB	108 2		628 2	112 1		109 1	355 2	376 1	381 1	381 1	497 1	502 2	1714 1	4367 1	182 2	236 2	397 1	398 2	578 2	751 2	894 2	969 2	1466 2	1995 1	4344 1	170 2	215 2	244 2	252 2	252 2	252 2
% Query Match	75.9	74.1	74.1	70.7	70.7	69.0	69.0	69.0	69.0	0.69	69.0	0.69	69.0	69.0		67.2	67.2	67.2	67.2	67.2	67.2	67.2	67.2	67.2	67.2	65.5		65.5	65.5	65.5	65.5
Score	44	43	43	41	41	40	40	40	40	40	40	40	40	40	39	39	39		39	39	39	39	39	39	39	38	38	38	38	38	38
Result No.		7	m	4	2	9	7	œ	0	10	11	12	13	14		16	17	18	19	20	21	.55	23	24	25	56	27	28	29	30	31

Q81x10 bacillus an Q6hbpl bacillus th Q7450 geobacter s Q8pln5 xanthomonas Q09205 caenorhabdi Q95649 streptomyce Q6788 sodalis glo Q76s2 molluscum c Q83155 molluscum c Q83155 molluscum c Q99591 mycobacteri Q7wz48 nonowuraea Q9wx6 candida alb P46005 escherichia P21672 saccharomyc
Q81XIO Q6HBP1 Q7HE50 D7PE50 DAPA_XANAC SRA3_CAEBL Q9FGD9 Q6R8A6 Q76S23 Q9B091 Q9B091 Q9B091 Q9B091 QPB15 Q9B091 Q9B091 AGG_ECOLI
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## ALIGNMENTS

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Gарв
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DBC-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin lambda light chain variable region (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                    [1] — SEQUENCE FROM N.A. MEDILO75; MEDILNE=98375893; PubMed=9712075; Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; "Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 75.9%; Score 44; DB 2; Local Similarity 72.7%; Pred. No. 3.1; les 8; Conservative 1; Mismatches
108 AA.
PRT;
                                                                                                                                                                                                                                                                                    antibody V region genes";
J. Immunol. 16:12020-2031(1998).
EMBL; U96394; AAB68783.1;
PDB; IXX4; Model; L=1-108.
InterPro; IPR007110; Ig-like.
InterPro; IPR00356; Ig-V.
ENART; EM0406; IGV; I.
PROSITE; PS50835; IG_LIKE; I.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Q96SB0
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Matches
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1 AAWDDSLSEFL 11 g ઠ

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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothical protein.
Homo sapiens (Human). 236 AA. PRT; PRELIMINARY; Q8NEJ1 RESULT 2 QBNEJ1 

emuco saptensa vameniu. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1] -SEQUENCE FROM N.A. TISSUE=Lung;

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LV1H HUMAN P06887;
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Rlausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Carannoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan K.J., Mala A.A., Guabarte P.H.,
Richards S., Worley K.C., Hale S., Garcianci P. Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garciance S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre B., Fairhead C., Ferry-Dumacet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Kluyveromyces lactis NRRL Y-1140.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.1%; Score 43; DB 2; Length 236; 100.0%; Pred. No. 11; 0; Indels iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lung;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0309984; AAH30984.1; -.
HSSP; P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ll protein.
236 AA; 25024 MW; 1703B77942630E08 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|O9HFC6 Yarrowia lipolytica Calnexin.
ORFNames=KLLAOF00462g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hypothetical protein.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-eet; I.
SMART; SM00406; IGv; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Q6CLT9
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Gaps
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--- MISCELLANEOUS: Residues 33-36 and some of the sequenced peptides
were positioned by homology.
--- MISCELLANEOUS: The C region of this chain has the Mcg+ and Kern+
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J. "Genome evolution in yeasts.";

Nature 430:35-44(2004).
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Mitheasco E., Roy J.D., Congy N., Peran-Rivat L., Mihaesco C.;
"The amino acid sequence of a lambda light chain presenting abnormal
physicochemical and antigenic features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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InterPro; IPkvv-
Pfam; PF00047; ig; 1.
SMART; SW00406; IGv; 1.
PROSITE; PS50815; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Monoclonal antibody; Pyrrolidone carboxylic acid.
NOMAIN 1 106 Ig-like.
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.1%; Score 43; DB 2; Length 628; 66.7%; Pred. No. 32; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, CR38126; CA697807.1; -.
GO, GO:0005514; F:calcium ion storage activity; IEA.
InterPro; IPR001580; Calret/Calnex.
InterPro; IPR001895; Cond like_lec_g1.
Figur, PF00262; Calreticulin; 1.
PRINTS; PR00626; Calreticulin; 1.
PROSTE; PS00803; CALRETICULIN.
PROSITE; PS00803; CALRETICULIN 1; 1.
PROSITE; PS00805; CALRETICULIN 1; 1.
PROSITE; PS00805; CALRETICULIN REPEAT; 1.
SEQUENCE 628 AA; 70981 MW; BODBA6D1A64644EE CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
01-JUL-2004 (Rel. 44, Last annotation update)
Ig lambda chain V-I region MEM.
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HSSP, P01703; 7PAB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 66.7
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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STRAIN=NRRL Y-1140;
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109 AAWDDSMS 116
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P04208;
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NON TER
SEQUENCE
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Q9A925;
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Matches
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A Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausher R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcherko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Jones M.J., Marra M.J.,
Jones M.J., Marra M.J.,
Jones M.J., Marra M.J.,
Jones M.J., Marra M.J
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                                                                                                                      Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                   Score 41; DB 1; Length 112;
Pred. No. 12;
                                                                                                                   2; Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
   112 AA; 11789 MW; 748124F079CFFBE4 CRC64;
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237 AA; 25108 MW; 6814170F7B784825 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                 237 AA
                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, BC075843; AAH75843.1; ...
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.-Il.
InterPro; IPR003596; Ig.-MHC.
InterPro; IPR003596; Ig.-V.
Pfam; PF07064; C1-set; I.
Pfam; PF070647; Ig. 2.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 1.
SWART; SW00406; IG; 1.
PROSITE; PS002599; IG.LIKE; 2.
PROSITE; PS002599; IG.MHC; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                      70.7%;
63.6%;
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Matches 7; Conservative
                                                                                                                7; Conservative
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                                                                                                                                                                                                              91 AAWDDSLDGYV 101
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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TISSUE-Primary B-Cells;
                                                                                                                                                                         1 AAWDDSLSEFL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
Homo sapiens (Human).
                                                         Query Match
Best Local Similarity
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   SO SEQUENCE
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MEDLINE=83221661; PubMed=6407018;
MEDLINE=83221661; PubMed=6407018;
Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
Takahashi Y., Takashi N., Tetaert D., Putnam F.W.;
Takahashi Y., Takashi N., Tetaert D., Putnam F.W.;
The lambda light chain.";
T
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STRAIN=ATCC 19089 / CB15;

MEDLINE=2113698; PubMed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE=21136998; PubMed=11259647; DOI=10.1073/pnas.061029298;

Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Pred. No. 18;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct protein sequencing; Immunoglobulin V region. DOMAIN V segment.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CC1169.
OrderedLocusNames=CC1169;
                                                                        20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
20-UIL-2004 (Rel. 44, Last annotation update)
Ig lambda chain V-I region WAH.
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109 AA
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PRT;
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STANDARD;
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89
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TIGE;

Matches

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RESULT

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SEQUENCE FROM N.A. (ISOFORM 2).
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 WDDSLSEFL 11
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69 WDDSMVEFM 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                       MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                            MUTAGEN
                                                                                                                                                                                                                                                                    DOMAIN
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CEA2_HUMAN
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-2201245; PubMed=12018390;
MEDLINE-2201245; PubMed=12018390;
Miltley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
Mittley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
Mittley P., Gibbard A.M., Mark and skeletal muscle.";
Identification of centaurin-alpha2: a phosphatidylinositide-binding
protein present in fat, heart and skeletal muscle.";
In Sur. J. Cell Biol. 81:222-230(202).
I. Eur. J. Cell Biol. 81:222-230(202).
I. Eur. J. Cell Biol. 81:222-230(202).
I. FUNCTION: GTPase-activating protein for the ADP ribosylation
C. I. SUBUNIT: Binds phosphatidylinositol 3, 4,5-terisphosphate (PrdInsP3) and inositol
Dissiphosphatidylinositol 3, 4,5-trisphosphate (PrdInsP3) and inositol
Dissiphosphate and phosphatidylinositol 3, 4-bisphosphate
C. I. SUBCELLULAR LOCATION: Cytoplasmic. Constitutively samilarity).
C. SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
C. SUBCELLULAR LOCATION: Excluded from the nucleus (By similarity).
C. ITSSUB SPECIFICITY: Expressed in many tissues, with highest levels
C. In fat. heart and skeletal muscle. Also detected in kidney, liver
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Sucopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., INTERACTION WITH PIDINS (4,5) P2, PIDINS (3,4,5) P3 AND INS (1,3,4,5) P4, TISSUE SPECIFICITY, AND MUTAGENESIS OF ARG-151 AND
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota, Metaroa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                                                                                                                                                                             Length 355;
                                                                                                                                                                                                                                                                                                                                                Indels
                   "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL; AE065795; AAK23153.1; -.
PIR; E87394; E87394.
                                                                                                                                                InterPro; IPR011251; Luciferase like.
Pfam; PF00296; Bac luciferase; I.
Complete proteome; Hypothetical protein.
SEQUENCE 355 AA; 38552 MW; 3C4AEF428255557 CRC64;
                                                                                                                                                                                                                                                                                          69.0%; Score 40; DB 2;
87.5%; Pred. No. 63;
cive 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARÏTY: Contains 1 Arf-GAP domain.
-!- SIMILARITY: Contains 2 PH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGD; 708497; LOC56836.
InterPro; IPR001164; hRIP_like.
InterPro; IPR001849; PH.
InterPro; IPR011036; PH_related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ238993; CAB88403.1; -.
                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 SAWDDSLS 145
                                                                                                                                                                                                                                                                                                                                                                                                      1 AAWDDSLS 8
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Centaurin alpha 2.
                                                                                                                               CC1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Centa2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEA2 RAT
                                                                                                                                                                                                                                                                                             Query Match
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SECUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20304757; PubMed=10843809; DOI=10.1006/geno.2000.6179;
Jenne D.E., Tinschert S., Stegmann E., Reimann H., Nurnberg P.,
Horn D., Naumann I., Buske A., Thiel G.;
"A common set of at least 11 functional genes is lost in the majority of NF1 patients with gross deletions.";
Genomics 66:93-97(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Leukocyte;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
MEDILINE=22012451, PubMed=12018330;
Whitley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour B.E.,
Prestwich G.D., Holman G.D.;
"Identification of centaurin-alpha2: a phosphatidylinositide-binding
protein present in fat, heart and skeletal muscle.";
Eur. J. Cell Biol. 81:222-230(2002).
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                    PH 2.
R->C: Almost complete loss of InsP4
binding.
R->C: No loss of InsP4 binding, Almost
complete loss of InsP4 binding; when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                            Repeat; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
SEQUENCE FROM N.A. (ISOFORM 1).
Bertsch U., Illies C., Mayr G.W.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                             376 AA; 43524 MW; E357392F38F07166 CRC64;
                                                                                                                                                                                                                                                                                          associated with C-15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9NPF8; Q8N4Q6; Q96SD5; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     69.0%; Sco. 66.7%; Pred. No. b.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 AA
PRINTS; PRO0405; REVINTRACTNG.
SMART; SM00105; ArfGap; 1.
SWART; SM0023; PH; 2.
PROSITE; PS501015; ARFGAP; 1.
PROSITE; PS50003; PH_DOMAIN; 2.
GTPASE activation; Metal-binding; Reper
                                                                                                                                                C4-type.
PH 1.
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villano D.K., Muzny D.M., Sodergren E.J., iux K., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9NPF8-2; Sequence=VSP_011180; Note=May be due to a competing acceptor splice site. No experimental confirmation available; TISSUE SPECIFICITY: Highly expressed in placenta, spleen, kidney, selected in muscle and adrenal gland. Weakly expressed in Infyroid, liver, heart, lung, small intestine, peripheral blood leukocytes. Not detected in spinal cord, brain, stomach, trachea, colon, lymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with the plasma membrane. Excluded from the nucleus.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50115; ARFGAP; 1.
PROSITE; PS50003; PH DOMAIN; 2.
Alternative splicing; GTPase activation; Metal-binding; Repeat; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanck T., Stricker R., Sedehizade F., Reiser G.; localization of "Identification of gene structure and subcellular localization of human centaurin alpha 2, and p42IP4, a family of two highly homologous, Ins 1,3,4,5-P4-/PtdIns 3,4,5-P3-binding, adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: GTPase-activating protein for the ADP ribosylation
factor family (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a stoichiometry of two binding sites for InsP4 with identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH PTDINS (3,4,5) P3 AND INS (1,3,4,5) P4, TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.

Pubmed=14690521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 Arf-GAP domain. SIMILARITY: Contains 2 PH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9NPF8-1; Sequence=Displayed;
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InterPro; IPR01849; PH.
InterPro; IPR011036; PH related.
Pfam; PF01412; ArfGap; I.
Pfam; PF00169; PH; 2.
PRINTS; PR00405; REVINTRACTNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ238994; CAB88383.1; -. EMBL; AJ272195; CAB77266.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Neurochem. 88:326-336(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAC40651.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC033758; AAH33758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGNC:16487; CENTA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00105; ArfGap; 1.
SMART; SM00233; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      node and bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H-InvDB; HIX0013699; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ242782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins."
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STRAIN=FVB/N 1 TISSUE=Breast tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Magner L. Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Heish F.,

A Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Heish F.,

B Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Heish F.,

B Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

B Connetein M.J., Usdin T.B., Toshiyuki S., Carninol F., Scheetz T.E.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milting M., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywniski M.I., Skalska U., Smailus D.E.,

B Cherration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. 2011. U.S.A. 99:16899-16903 (2002).

-! FUNCTION: GTPage-activating protein for the ADP ribosylation factor family (Potential).

-! SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3) and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a stoichiometry of two binding sites for InsP4 with identical affinity (By similarity).

-! SUBCELLUIAR LOCATION: Cytoplasmic. Constitutively associated with the plasma membrane. Excluded from the nucleus (By similarity).

-! SIMILARITY: Contains 1 Aff-CAP domain.
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                       ö
                                                                                                                                                                           69.0%; Score 40; DB 1; Length 381; 66.7%; Pred. No. 68; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                FTId=VSP_011180.
-> P (in Ref. 3).
4FAE208072A92C01 CRC64;
Arf-GAP.

C4-type.

PH 1.

PH 2.

Missing (in isoform 2).

/FTIG=VSP 011180.

L -> P (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                       381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                          381 AA; 44348 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences."
                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                             3 WDDSLSEFL 11
                                                                                                                                                                                                                                                                                                   69 WDDSIVEFM 77
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Centaurin alpha 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
  25
132
255
269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Centa2;
                                                                                                                                                                                                                                                                                                                                                                                                     CEA2 MOUSE
Q8R2V5;
                                                          DOMAIN
VARSPLIC
                                                                                                                                          SEQUENCE
  DOMAIN
ZN FING
DOMAIN
                                                                                                                     CONFLICT
                                                                                                                                                                                                                     Matches
  SOTETTE
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There are no restrictions on
                                                                                                                                                                  EMBL; AL591985; CAC49535.1; -.
EMBL; AP080548; AAD12735.1; -.
EMBL; AP080548; AAD12735.1; -.
EMBL; AP080548; AAD12735.1; -.
EMBL; PO8859; G19583.
HAMAP; MF 00186; -; 1.
InterPro; IPR000577; FGGY kin.
InterPro; IPR00599; G1ycerol_kin.
Ffam; PF0370; FGGY_C; 1.
Pfam; PF0370; FGGY_C; 1.
Pfam; PF0370; FGGY_N; 1.
PROSITE; PS00933; FGGY_KINASES_1; FALSE_NEG.
PROSITE; PS00445; FGGY_KINASES_2; 1.
ATP-binding; Complete proteome; G1ycerol metabolism; Kinase; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.0%; Score 40; DB 2; Length 502; 60.0%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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Juerchott K., Boerner T.;
Juerchott K., Boerner T.;
Juerchott K., Boerner T.;
Juerchott K., Boerner T.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
EMBL, 22837; CA82191-1; -.
PIR, 549113; S49113.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR007936; VirE.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE 502 AA; 58859 MW; 98E6ID5CZ14520E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 165 ATP (Probable).
497 AA; 54419 MW; 42D342B335ACC2B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Cyanobacteria; Chroococcales; Microcystis
NCBI_TaxID=1126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.0%; Score 40; DB 1; 70.0%; Pred. No. 90; tive 1; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 32, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Putative helicase C28H8.3 (EC 3.6.1.-).
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European Bioinformatics Institute.
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434 SWEDELAEFL 443
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nes 7; Conserv
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01-NOV-1996 (
01-MAR-2004 (
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Q09475;
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SEQUENCE
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Q48904;
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YP93_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILNE-21396508; PubMed-11481431; DOI=10.1073/pnas.161294698; Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.;

"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti."; Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE=99121023; PubMed=9922248;
MEDLINE=99121023; PubMed=9922248;
Aneja P., Charles T.C.;
"Poly-3-hydroxybutyrate degradation in Rhizobium (Sinorhizobium)
meliloti: isolation and characterization of a gene encoding 3-
hydroxybutyrate dehydrogenase.";
J. Bacteriol. 181:849-857(1999)
-1- FUNCTION: Key enzyme in the regulation of glycerol uptake and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY 2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Glycerol kinase (EC 2.7.1.30) (ATP:Glycerol 3-phosphotransferase)
(Glycerokinase) (GK).
Rame=glpK, OrderotLocusNames=RB1135, ORFNames=SMD21009;
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2)
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-!- CATALYTIC ACTIVITY: ATP + glycerol = ADP + sn-glycerol 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphate.
--- PATHWAY: Glycerol utilization; rate-limiting step.
--- SIMILARITY: Belongs to the fucokinase / gluconokinase / glycerokinase / xylulokinase family.
                                                                                                                                                                                                                                                                                                   SMART; SMOUZJJ; F.H. ARFGAP; 1.
PROSITE; PSSOUJS; PH DOMAIN; 2.
GTPase activation; Metal-binding; Repeat; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; froteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 1; Length 381;
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2E504CEF0ACD84D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           497 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                C4-type.
PH 1.
                                                          MGD; MGI:2663075; Centa2.
InterPro; IPR001164; hRIP_like.
InterPro; IPR001164; PH related.
InterPro; IPR011036; PH related.
Pfam; PF001412; ArfGap; I.
Pfam; PR00169; PH; 2.
PRINTS; PR00105; REVINTRACTNG.
SNART; SM00105; ArfGap; 1.
                                    EMBL; BC027165; AAH27165.1; -.
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Best Local Similarity 66.7
Matches 6; Conservative
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233
361
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132 2
255 3
381 AA;
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086033;
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GLPK_RHIME
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ORFNames=C28H8.3;
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=74-0R23-1A / FGSC 987;
MEDLINE=95014704; Pubmed=7929559; DOI=10.1083/jcb.127.1.139;
Plamann M., Minke P.F., Tinsley J.H., Bruno K.S.;
"Cytoplasmic dynein and actin-related protein Arpl are required for
                                                                                                                                                                                 Waterston R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: Belongs to the helicase family. SKI2 subfamily.
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                                                                                   STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1; Length 1714; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                         InterPro; IRR001410; DEAD.
InterPro; IRR001410; DEAD.
InterPro; IRR001410; DEAD.
InterPro; IRR001650; Helicase_C.
Pfam; PF00271; Helicase C; 1.
SMART; SM00487; DEXDC; T.
SMART; SM00489; HELICC; T.
ATP-binding; Helicase; Hydrolase; Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
(Potential).
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ATP (Poten
DEVH box.
                                                                                                                                                                                                                                                                                                                                         EMBL; U20861; AAA62291.2; -.
WormBase; WBGene00016194; C28H8.3.
WormPep; C28H8.3; CE29195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.98;
                                                                                                                                    investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614
813
916
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Best Local Similarity
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                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein.
                                                 NCBI_TaxID=6239;
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DYHC NEUCR
DYHC NEUCR
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DT 01-NOV
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DB Dynein
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OC SURARY
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CC STRAIN
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RP SEQUENCE FROM N.A.

RP STONEST STAIN=74-0823-1A FOSC 987;
RATAN=74-0823-1A FOSC 987;
RATAN=74-0823-1A FOSC 987;
RATAN=74-0823-1A FOSC 987;
RATAN=74-0823-1A FOSC 987;
RA Galegan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Redman B.,
RA Jaffe D., Faltzhigh W., Ma L.-J., Smirnov S., Putterel S., Rehman B.,
RA Hins T., Engels R., Wang S., Nieleen C.B., Butler J., Endrizzi M.,
RA Bikins T., Engels R., Wang S., Nieleen C.B., Butler J., Endrizzi M.,
RA Stanger-Thomann M., Selltremnikoff C.P., Kinsey J.A., Braun E.L.,
RA Ratener Washburne M., Selltremnikoff C.P., Kinsey J.A., Braun E.L.,
RA Marcotte E., Greenberg D., ROY A., Folly K., Naylor J.,
RA Ramussen C., Metzenberg D., ROY M., Folly K., Naylor J.,
RA Maccott E., Greenberg D., Li W., Pratt R.J., Ommani S.,
RA Maccoli E., Metzenberg E., Frishman D., Krystoffows S.,
RA Maccoli E., Metzenberg E., Perkins D.D., Kroken S., Cogoni C.,
RA Maccin G., Carcheside D., Li W., Pratt R.J., Ommani S.A.,
RA Nature J.D., Alex L., Penkins D.D., Kroken S.,
RA Macino G., Carcheside D., Li W., Pratt B.J., Ommani S.,
RA Macino G., Carcheside D., Li W., Pratt B.J.,
RA Match D., Alex L., Mannhaupt G., Ebbole D.J., Fraitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
Ruture 422:859-868(2003).
RA Transon M.S., Lander E.S., Nusbaum C., Birren B.,
Ruture 422:859-868(2003).
RA Transon M.S., Lander E.S., Nusbaum C., Birren B.,
Ruture 422:859-868(2003).
RA Transon M.S., Lander E.S., Nusbaum C., Birren B.,
Ruture 422:859-868(2003).
Ration M.S., Lander E.S., Nusbaum C., Birren B.,
Ruture 422:859-868(2003).
Ration M.S., Lander E.S., Maccomposer atroke is Dynain has ATPase activity; the force-producing power stroke is Unogin has ATPase activity; the force-producing power stroke is Unogin has ATPase activity; the force-producing power stroke is uncertainted of all lands two heavy chains and a number of Lowann L. Downin: Dynain heavy chains probably consist of an N-terminal stem (Which binds cargo and interacts with other dynain components).

RA SUBBULL Dynain heavy chain
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1904 Stem (By similarity).
2130 AAA 1 (By similarity).
2815 AAA 3 (By similarity).
2815 AAA 4 (By similarity).
3179 AAA 4 (By similarity).
3179 AAA 6 (By similarity).
4215 AAA 6 (By similarity).
693 Coiled coil (Potential).
1215 Coiled coil (Potential).
1574 Coiled coil (Potential).
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mal nuclear distribution in filamentous fungi."; Cell Biol. 127:139-149(1994).
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR004273; Dynēin heavy.
PF03028; Dynein heavy.
SWART; SW00382; AAA, 3.
ATP-binding; Coiled coil; Dynein; M
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SEQUENCE FROM N.A.

STAIN-RIMD 2210633 / Serotype 03:K6;

MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

MAXINO K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";

Lancet 361:743-749(2003).

EMBL; AR065088; BAC65255.1; -.

Complete proteome; Hypothetical protein.

SEQUENCE 182 AA; 21333 MW; 2559BEC89FD78332 CRC64;
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Pred. No. 9.3e+02;
2; Mismatches 1; Indels
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Vibrionaceae, Vibrio.
NCBI_TaxID=670;
2218 Coiled coil (Potential).
2218 Coiled coil (Potential).
3296 Coiled coil (Potential).
3481 Coiled coil (Potential).
3809 ATP (Potential).
2247 ATP (Potential).
2612 ATP (Potential).
2612 ATP (Potential).
2654 ATP (Potential).
265568 MW, 1810F3E2D170bGDF CRC64;
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01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein VPA1212.
OrderedLocusNames=VPA1212;
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Matches 6; Conservative
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Matches 5; Conservative
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455 AWDESIKEF 463
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Search completed: October 14, 2005, 16:19:59 Job time : 75.2188 secs

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                                                                                                                                                                                                                        October 14, 2005, 16:00:04; Search time 21.6562 Seconds (without alignments) 37.917 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-350-260A-374
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US-08-5115-574-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                             OM protein
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
No.
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Sequence 112, App
Sequence 113, App
Sequence 114, App
Sequence 5, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 40, Appli
Sequence 40, Appli
Sequence 40, Appli
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                                                                                                                                                      Sequence 40, Appl
Sequence 361, App
Sequence 446, App
Sequence 514, App
Sequence 361, App
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                                                                                                                                                                                                                                                                   Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 58; DB 4; L
100.0%; Pred. No. 0.00037;
iive 0; Mismatches 0;
US-09-315-574-39
US-08-211-202-113
US-08-211-202-113
US-09-212-202-5
US-09-315-574-5
US-09-956-086-4
US-09-956-088-4
US-09-985-442-7
US-09-985-442-7
US-09-985-442-7
US-09-985-442-7
US-09-985-442-7
US-09-985-444-40
US-08-350-260A-361
US-08-350-260A-361
US-08-350-260A-361
US-08-350-260A-361
US-08-350-260A-361
US-08-350-260A-361
US-08-350-260A-361
US-08-350-260A-314-00
                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-08-273-146-63
is Sequence 63, Application US/08273146
is Patent No. 585585
is GENERAL INFORMATION:
APPLICANT: Smith, Rodger
APPLICANT: McCafferty, John
APPLICANT: Chiswell, David
APPLICANT: Pitzgerald, Kevin
APPLICANT: Fitzgerald, Kevin
APPLICANT: Fitzgerald, Kevin
APPLICANT: Martin, Mark T.
APPLICANT: ATITMAS, Richard C.
APPLICANT: Titmas, Richard O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
  1 AAWDDSLSEFL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-383-667-15
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02-DEC-1991
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-08-350-260A-374
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Sequence 15, Application US/08652816A

Patent No. 587215

GENERAL INFORMATION:

APPLICANT: Osbourn, JK

APPLICANT: McGafferty, JG

TITLE OF INVENTION: Specific binding members, materials and

TITLE OF INVENTION: Methods.

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

COMPUTRY: United States of America

COMPUTRY: United States of America

COMPUTRY: Inhinois

COMPUTRY: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE PLANGALION NATA:

APPLICATION NUMBER: US/08/652,816A

FILING APPLICATION DATA:

APPLICATION NUMBER: GB 9125579.4

FILING APPLICATION NUMBER: GB 02-DEC-1991
     The Isolation and Production of Catalytic Antibodies using Phage Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-7UL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RYAM. JOHN W.
REGISTRATION NUMBER: 09000
TELECHMONICATION INFORMATION:
TELEFRAK: 301-294-8000
TELEFRAK: 301-294-8000
TITLE OF INVENTION: The Isolation a TITLE OF INVENTION: Catalytic Antib NUMBER OF SEQUENCES: 71 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ISSU East Jefferson St. CITY: Rockville STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 63: SEQUENCE CHARACTERISTICS: LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-273-146-63
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APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: binding pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25 (BPO)
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bartnicki, Audrey L.
REGISTATION WUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 4;
Pred. No. 0.05;
                                                                          PILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 14-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INCRMATION:
APPLICATION NUMBER: US/09/104,337A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                            APPLICATION NUMBER: US 08/350,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 374: US-09-104-337A-374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 346, Application US/08350260A; Patent No. 5962255; GENERAL INFORMATION:
                  FILING DATE: 25-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.3%;
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-350-260A-346
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Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 600
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MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 2; Length 11;
Pred. No. 0.05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
                                                                                                                                                                                                                                              FILING APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/GB93/00605
RILING DATE: 24 MAR-1993
PRIOR APPLICATION NUMBER: US 08/150,002
APPLICATION NUMBER: US 08/150,002
RILING DATE: 31 MAR-1994
PRIOR APPLICATION DATA: 31 MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY-AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 374, Application US/09104337A
Patent No. 6492160
GENERAL INPORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
             APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
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COUNTRY: USA
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Best Local Similarity
Matches 8; Conserv
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Gaps

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Sequence 60, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
THOSE SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0.11;
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COUTRY: USA
ZIP: 94111-4834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
7111NG DATE: 13-UNN-1996
                 PRIOR APPLICATION NOMBER: US/09/104,33/A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 12-MAY-1992
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 12-MAY-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1993
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/350,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGBNT INFORMATION:
NAME: BATTON NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGBNT INFORMATION:
NAME: BATTON NUMBER: US 08/307,619
FILING DATE: 10-SEP-1994
ATTORNEY/AGBNT INFORMATION:
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 346:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION
FILING DATE: 13-JUN-1220
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION UNBER: US 60/000,250
APPLICATION NUMBER: US 60/000,250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.9%;
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Best Local Similarity 72...
Best Local Similarity 72...
8; Conservative
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US-08-665-202-60
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Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
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COMPUTER READABLE FORM:

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.9%; Score 44; DB 2; Length 11; 72.7%; Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                   APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY 1991
RION APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: BPLICATION DATA: BPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR.1992
RION APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
RION APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
RION APPLICATION NUMBER: BCT/GB93/00605
FILING DATE: 31-MAR-1993
RION APPLICATION NUMBER: BCT/GB93/00605
FILING DATE: 31-MAR-1993
RION APPLICATION NUMBER: BCT/GB93/00605
FILING DATE: 18-MAR-1994
RILING DATE: 16-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-MAR-1994
APPLICATION NUMBER: BCT/GB93/00605
FILING DATE: 16-MAR-1994
APPLICATION NUMBER: BCT/GB93/07,619
FILING DATE: 16-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28111/32372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 346, Application US/09104337A Patent No. 6492160 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterhouse, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Clough, David W
REGISTRATION UNDHER: 36.107
REFERENCE/DOCKET NUMBER: 28111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312.474-6300
INFORMATION FOR SEQ 1D NO: 346:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAWDDSLSEFL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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US-08-350-260A-346
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MOLECULE TYPE: peptide
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chicago
                            US-09-315-574-60
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APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEB: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Rour Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                     Query Match 74.1%; Score 43; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
PRIOR APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/65,202
FILING DATE: 13-JUN-1995
APPLICATION NUMBER: US 08/665,202
RILING DATE: 13-JUN-1996
ATTONENLARENT INFORMATION:
              NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCK-DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
FILEPRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-315-574-60
; Sequence 60, Application US/09315574
; Patent No. 6512097
ATTORNEY/AGENT INFORMATION:
NAME: Hunter. Tom
                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-08-665-202-60
                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAWDDSLS 8
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Query Marchae (14.14) Score 43, DB 41 Length 9;
Marches 8: Conservative 0, Mismarches 0; Indels 0; Gaps 0);
Marches 8: Conservative 0, Mismarches 0; Indels 0; Gaps 0);
Mannaches 8: Conservative 0, Mismarches 0; Indels 0; Gaps 0);
Mannaches 8: Conservative 0, Mismarches 0; Indels 0; Gaps 0);
Mannaches 13: Application US/08150260A
| Mannaches 13: Application US/08150260A
| Marches 14: Application US/08150A
| Marches 14: Application US/08150A
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Gaps
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Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
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CURRENT APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A

FILING DATE: 25-Jun-1998

PRIOR APPLICATION NUMBER: US 08/350,260

FILING DATE: 15-MAY-1991

APPLICATION NUMBER: US 08/350,44

FILING DATE: 15-MAY-1991

APPLICATION NUMBER: GB 9210549.4

FILING DATE: 15-MAY-1991

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 24-MAR-1992

APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993

APPLICATION NUMBER: US 08/150,002
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                    Length 10;
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bartnicki, Audrey L.
REGISTATION WUMBER: 40,499
REPERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    Score 43; DB 2;
Pred. No. 0.15;
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 339, Application US/09104337A Patent No. 6492160 GENERAL INFORMATION:
                                                                                                                                                                                   74.1%; Sco.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606-5402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 10 amino acids
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                   Conservative
                                                                                                                  single
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                                                                                                                                                                               Query Match
Best Local Similarity
'''' 8; Conserve
                                                                                        TYPE: amino acid;
STRANDEDNESS: sir;
TOPOLOGY: linear
US-08-350-260A-497
                                                                                                                                                                                                                                                                                               1 AAWDDSLS 8
                                                                                                                                                                                                                                                                                                                                       1 AAWDDSLS 8
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                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Sequel Cameron
APPLICANT: Nissim, Ahuva
APPLICANT: Nissim, Ahuva
APPLICANT: Smith, Andrew John Hammond
ITTLE OF INVENTION: Methods for producing members of specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DINGING PAIRS
TITLE OF INVENTION: DINGING PAIRS
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 6606-6402
COMBUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
RRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 15-MAY-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
RRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 34-MAR-1994
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: US 08/307,619
                                                                                                                                     DB 2; Length 10; 0.15;
                                                                                                                                                                                 0; Indels
                                                                                                                                                                                 0; Mismatches
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REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
                                                                                                                                     74.1%; Score 43; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                            US-08-350-260A-497; Sequence 497, Application US/08350260A; Patent No. 5962255
  LENGTH: 10 amino acids
                                                                                                                              Query Match
Best Local Similarity 100.
Matches 8; Conservative
                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                              1 AAWDDSLS 8
                                                                                                                                                                                                                                                          1 AAWDDSLS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                        ; TOPOLOGY: 1
US-08-350-260A-339
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Gaps

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Length 10; Indels

DB 4;

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: PC-DOS/MS-DOS
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 105-DBC-1994
CLASSIFICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
RAPPLICATION NUMBER: GB 9206318.9
FILING DATE: 34-MAR-1992
FILING DATE: 34-MAR-1992
FILING DATE: A4-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                     74.1%; Score 43; DB 100.0%; Pred. No. 0.1 tive 0; Mismatches
; SEQUENCE DESCRIPTION: SEQ ID NO: 497: US-09-104-337A-497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARION APPLICATION DATA

AND APPLICATION NUMBER: PCT/GB91/01134

FILING DATE: 10-JUL-1991

REIGN APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 15-MAY-1992

RIGN APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993

RIGN APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002

FILING DATE: 31-MAR-1994

RIGN APPLICATION NUMBER: US 08/307,619

FILING DATE: 16-SEP-1994

ATTONNEY/AGENT INPORMATION:
NAME: CLOUGH, DAVIG W

REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28111/32372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                     Query Match 74.1
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicago
                                                                                                                                                          1 AAWDDSLS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60606-6402
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Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific binding pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCHUTER: FLOPEY GIRK
COMPUTER: FLOPEY GIRK
COMPUTER: FLOPEY GIRK
COMPUTER: BY PC COMPACTION
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 910549.4
FILING DATE: 15-MAX-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 15-MAX-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 24-MAX-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 15-MAY-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
APTLORING DATE: 16-SEP-1994
ATTORNEY/AGENT INPORMATION: PARTING DATE: 16-SEP-1994
ATTORNEY/AGENT INPORMATION: PARTING DATE: 16-SEP-1994
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ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                 74.1%; Score 43; DB 4; Length 10; 100.0%; Pred. No. 0.15; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-104-337A-497
; Sequence 497, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Waterhouse, Peter
; Nissim, Ahuva
    TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 339:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                           1 AAWDDSLS 8
                                                                                                                                                                                                                                                      1 AAWDDSLS 8
                                                                                                                                                        Best Local Similarity
Matches 8; Conserv
                                                                                         US-09-104-337A-339
                                                                                                                                      Query Match
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Job time : 21.6562 secs

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                                     Query Match 74.1%; Score 43; DB 2; Length 11; Best Local Similarity 100.0%; Pred. No. 0.17; Matches 8; Conservative 0; Mismatches 0; Indels
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 8; Conservative
     ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY:
US-08-350-260A-441
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MOLECULE TYPE: peptide
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1 AAWDDSLS 8
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Search completed: October 14, 2005, 16:22:03

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RESULT
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Sequence 1927, Ap
Sequence 29, Appl
Sequence 33, Appl
Sequence 1926, Ap
Sequence 1926, Ap
Sequence 1926, Ap
Sequence 3241, Ap
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                                                                                                                           October 14, 2005, 16:20:10; Search time 78.2031 Seconds (without alignments) 58.615 Million cell updates/sec
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Sequence 40,
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-981-692-40
US-09-880-748-1927
US-10-293-418-1927
US-10-981-692-29
US-10-981-692-26
US-10-981-692-26
US-10-2981-692-26
US-10-293-418-1926
US-10-293-418-1926
US-10-293-418-1926
US-10-293-418-3241
US-10-981-692-31
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                                                                                                                                                                                                                                                                                                                                                                      1859788 segs, 416717961 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - protein search, using sw model
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seq length: 200000000
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58
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Maximum DB
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1419, AP
1618, AP
2049, AP
2065, AP
1419, AP
1618, AP
2049, AP
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US-09-880-748-1913

US-10-293-418-1917

US-10-293-418-1917

US-09-880-748-1443

US-09-880-748-148-1929

US-09-880-748-1929

US-09-880-748-1929

US-09-880-748-1929

US-10-293-418-1929

US-10-293-418-1618

US-10-293-418-1618

US-10-293-418-1618

US-10-293-418-1618

US-10-293-418-2049

US-10-293-418-2049

US-10-293-418-2049

US-10-293-418-2049

US-10-293-418-2049

US-10-293-418-2049

US-10-293-418-2049

US-10-293-418-2049

US-11-017-030-148-2049

US-11-017-030-14
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US-10-981-692-24

; Sequence 24, Application US/10981692
; Publication NO. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR PAPLICATION NUMBER: PC7/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR APPLICATION NUMBER: 60/383,802
; RIOR APPLICATION NUMBER: 50/383,802
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 24
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
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hes 11; Conservative
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RESULT 5
US-10-981-692-29
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Sequence 40, Application US/10981692
| Publication No. US20050163777A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B | TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B | FILE REFERENCE: PF590P1 |
| CURRENT APPLICATION NUMBER: US/10/981,692 |
| CURRENT FILING DATE: 2004-11-05 |
| PRIOR APPLICATION NUMBER: PC7/US03/16802 |
| PRIOR FILING DATE: 2003-05-29 |
| PRIOR FILING DATE: 2003-05-29 |
| PRIOR FILING DATE: 2003-05-29 |
| PRIOR FILING DATE: 2003-05-30 |
| NUMBER OF SEQ ID NOS: 76 |
| SOFTWARE: PatentIn version 3.1
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR PLILOG DATE: 2000-10-17

PRIOR PLILOG DATE: 2001-03-16

PRIOR PLILOG DATE: 2001-03-16

PRIOR PLILOG DATE: 2001-03-16

PRIOR PLILOG DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PLILOG DATE: 2001-03-21

PRIOR PLILOG DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOUTHARE: PREDERING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOUTHARE: PREDERICATION VARIER: 60/293,499

PRIOR PLILOG DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SEQ ID NO 1927
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100.0%; Score 58; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
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US-09-880-748-1927
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LENGTH: 242
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Publication No. US20050163777A1
GENERAL INFORMATION:
APPLICANT: ROSE et al.
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PF590P1
CURRENT PAPLICATION NUMBER: US/10/981,692;
CURRENT FILING DATE: 2004-11-05;
PRIOR APPLICATION NUMBER: PCT/US03/16802;
PRIOR APPLICATION NUMBER: 60/383,802;
PRIOR APPLICATION NUMBER: 60/383,802;
PRIOR APPLICATION NUMBER: 60/383,802;
RIOR APPLICATION NUMBER: 60/383,802;
RIOR APPLICATION NUMBER: 60/383,802;
RIOR APPLICATION NUMBER: 2002-05-30;
NUMBER OF SEQ ID NOS: 76;
SOFTWARE: PatentIn version 3.1;
LENGTH: 243
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### APPLICANT: Ruben et al.

### TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT PILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/311,469
PRIOR PILING DATE: 2001-11-16
PRIOR PLICATION NUMBER: 60/340,817
PRIOR PLICATION NUMBER: 60/340,817
PRIOR PLICATION NUMBER: 60/293,499
PRIOR PLICATION NUMBER: 60/293,499
PRIOR PLING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR PLILNG DATE: 2001-03-16
PRIOR PLING DATE: 2000-01-17
PRIOR PLILNG DATE: 2000-06-16
NUMBER: 60/212,210
PRIOR PLILNG DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
LENGTH: 241
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100.0%; Score 58; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
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US-10-981-692-29
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US-10-293-418-1927
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Best Local Similarity
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RESULT 6 US-10-981-692-33

RESULT 4
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US20030223996A1

2001-06-15

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US-10-293-418-3241
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Sequence 33, Application US/10981692
Publication No. US20050163777A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILE REPERENCE: PF590P1
CURRENT FILING DATE: 2004-11-05
PRIOR FILING DATE: 2004-11-05
PRIOR PLICATION NUMBER: PCT/US03/16802
PRIOR FILING DATE: 2004-12-05
PRIOR FILING DATE: 2004-05-29
PRIOR PLICATION NUMBER: 60/383,802
PRIOR PLICATION NUMBER: 60/383,802
PRIOR PLICATION NUMBER: 60/383,802
PRIOR PRIOR PRIOR DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
LENGTH: 243
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| Sequence 26, Application US/10981692
| Sequence 26, Application US/10981692
| Publication No. US2005016377A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PFS90P1
| CURRENT APPLICATION NUMBER: US/10/981,692
| CURRENT APPLICATION NUMBER: US/10/981,692
| PRIOR PILING DATE: 2004-11-05
| PRIOR PILING DATE: 2004-05-29
| PRIOR PILING DATE: 2002-05-30
| NUMBER OF SEQ ID NOS: 76
| SEQ ID NO 26
| SEQ ID NO 26
| LENGTH: 244
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Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENDENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 58; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
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; Pred. No. 0.048;
0; Mismatches 0; Indels
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US-10-981-692-26
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: N023E01 scFv
US-10-981-692-33
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Best Local Similarity 100.0%;
Matches 11; Conservative 0
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Gaps
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Sequence 1926, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICATY: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

FILE REFERENCE: PF523P2

FRIOR APPLICATION NUMBER: 60/331,469

FRIOR PILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR PILING DATE: 2001-01-09

FRIOR PILING DATE: 2001-06-15

FRIOR PILING DATE: 2001-06-15

FRIOR PILING DATE: 2001-05-25

FRIOR PILING DATE: 2001-01-16

FRIOR PILING DATE: 2001-01-01-17

FRIOR PILING DATE: 2001-01-17

FRIOR PILING DATE: 2001-01-17

FRIOR PILING DATE: 2000-10-17

FRIOR PILING DATE: 2000-10-17

FRIOR FILING DATE: 2000-10-17

FRIOR FILING DATE: 2000-10-17

FRIOR FILING DATE: 2000-06-16

FRIOR FILING DATE: 2000-06-16
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100.0%; Score 58; DB 10; Length 2
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PELLING DATE: 2000-10-17
PRIOR PELLING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR PRIOR PELLING DATE: 2001-03-21
PRIOR PELLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SEQ ID NO 1926
LENGTH: 245
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Best Local Similarity 100.
Matches 11; Conservative
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CAGANISM: Homo sapiens
US-09-880-748-1926
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; ORGANISM: Homo sapiens
US-10-293-418-1926
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                                               GENERAL INVOCATION:

GENERAL INVOCATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR PLICATION NUMBER: 60/331,469

PRIOR PLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/290,817

PRIOR PILING DATE: 2001-6-15

PRIOR PLILING DATE: 2001-6-15

PRIOR PLILING DATE: 2001-6-15

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-16

PRIOR PLILING DATE: 2001-03-16

PRIOR PLILING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17
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TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin E TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin E CURRENT APPLICATION NUMBER: US/10/981,692
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR PILING DATE: 2003-65-29
PRIOR PILING DATE: 2002-65-30
PRIOR FILING DATE: 2002-05-30
SOFTWARE: Patentin version 3.1
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; Sequence 31, Application US/10981692

; Publication No. US20050163777A1

; GENERAL INFORMATION:
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Publication No. US20030223996A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 AAWDDSLSEFL 234
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US-10-293-418-3241
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LENGTH: 245
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; TILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT PILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR PILING DATE: 2000-10-17
; PRIOR PILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR PILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR PILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR PILING DATE: 2001-03-16
; PRIOR PILING DATE: 2001-03-21
; PRIOR PILING DATE: 2001-03-25
; NUMBER OF SEQ ID NOS: 3239
; SEQ ID NOS: 3239
Sequence 1913, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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                                                                                                                                                    TITLE OF INVENTION: ARCHIOCOLES LIGG. THE REFERENCE: PF5.23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATECHIN VET: 2.0
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Best Local Similarity luv.
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CORGANISM: Homo sapiens
US-09-880-748-1913
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US-09-880-748-1917
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US-10-293-418-1917

Query Match

Best Local Similarity 100.0%; Score 58; DB 15; Length 246;

Best Local Similarity 100.0%; Pred. No. 0.049;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11

Db 225 AAWDDSLSEFL 235

Search completed: October 14, 2005, 17:00:44
Job time: 78.2031 secs
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